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FIGURE 238

MMSFLLGAILTLLWAPTAQAEVLLQPDFNAEKFSGLWYVVSMA SDCRVFLGKKDHLSMSTRAI
RPTEEGGLHVHMEFPGADGCNQVDAEYLKVGSEGHFRVPALGYLDVRIVDTDYSSFAVLYIYK
ELEGALSTMVQLYSRTQDVSPQALKSFQDFYPTLGLPKDMMVMLPQSDACNPESKEAP

Signal peptide:

amino acids 1-20

Tyrosine kinase phosphorylation site.

amino acids 110-117

N-myristoylation sites.

amino acids 7-13, 79-85, 130-136

Amidation site.

amino acids 50-54

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FIGURE 239

GGCGCGCTGGTCCAGGTGAGCGGGCGCGTCCCCGCGACGGCGCTGCCTGCCCCGAGGCGGTTCA
CGTAAAGACAGCGAGATCCTGAGGGCCAGCCGGGAAGGAGGCGTGGATATGGAGCTGGCTGCT
GCCAAGTCCGGGGCCCGCGCCGCTGCCTAGCGCGTCTTGGGGACTCTGTGGGGACGCGCCCCG
CGCCGCGGCTCGGGGACCCGTAGAGCCCGGCGCTGCGCGCATGGCCCTGCTCTCGCGCCCCGC
GCTCACCCCTCCTGCTCCTCCTCATGGCCGCTGTTGTCAGGTGCCAGGAGCAGGCCAGACCAC
CGACTGGAGAGCCACCCTGAAGACCATCCGGAACGGCGTTCATAAGATAGACACGTACCTGAA
CGCCGCTTGGACCTCCTGGGAGGCGAGGACGGTCTCTGCCAGTATAAATGCAGTGACGGATC
TAAGCCTTTCCACGTTATGGTTATAAACCTCCCCACCGAATGGATGTGGCTCTCCACTGTT
TGGTGTTCATCTTAACATTGGTATCCCTTCCCTGACAAAGTGTGCAACCAACACGACAGGTG
CTATGAGACCTGTGGCAAAGCAAGAATGACTGTGATGAAGAATTCCAGTATTGCCTCTCAA
GATCTGCCGAGATGTACAGAAAACACTAGGACTAACTCAGCATGTTTCAGGCATGTGAAACAAC
AGTGGAGCTCTTGTTTGACAGTGTTATACATTTAGGTTGTAAACCATATCTGGACAGCCAACG
AGCCGCATGCAGGTGTCATTATGAAGAAAAAACTGATCTTTAAAGGAGATGCCGACAGCTAGT
GACAGATGAAGATGGAAGAACATAACCTTTGACAAATAACTAATGTTTTTACAACATAAACT
GTCTTATTTTTGTGAAAGGATTATTTTTGAGACCTTAAATAAATTTATATCTTGATGTTAAAC
CTCAAAGCAAAAAAAGTGAGGGAGATAGTGAGGGGAGGGCACGCTTGTCTTCTCAGGTATCTT
CCCCAGCATTGCTCCCTTACTTAGTATGCCAAATGTCTTGACCAATATCAAAAACAAGTGCTT
GTTTAGCGGAGAATTTTGAAAAGAGGAATATATAACTCAATTTTCACAACCACATTTACCAA
AAAAGAGATCAAATATAAAATTCATCATAATGTCTGTTCAACATTATCTTATTTGGAAAATGG
GGAATTATCACTTACAAGTATTTGTTTACTATGAAATTTTAAATACACATTTATGCCTAGAA
GGAACGGACTTTTTTTTTCTATTTTAATTACACATAATATGTAATTAAAGTACAACATAATAT
GTTGTTTCTCTGTAGCCCGTTGAGCATATGAGTAAGTCACATTTCTATTAGGACTACTTACAA
GGACAAGGTTTCCATTTTCCAGTTGTAAAATTGGAACCATCAGCTGATAACCTCGTAGGGAG
CAACCCAGGATAGCTAAGTGTTATGTAATATGCCTAGAAGGTGATGTGAATGCGATTGAGAA
GCATAGCCACTCCCATTTTATGAGCTACTCACATGACAAATGTCATCTTTTGCTATAACCTTT
GCCAAGTTAGAGAAAAGATGGATTTAATGAGATAAATGAAAAGATATTTAACCTAAAAA
AAAAAAAAAAAAAAAAA

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FIGURE 240

MALLSRPALTL L L L L L L M A A V V R C Q E Q A Q T T D W R A T L K T I R N G V H K I D T Y L N A A L D L L G G E D G L C
Q Y K C S D G S K P F P R Y G Y K P S P P N G C G S P L F G V H L N I G I P S L T K C C N Q H D R C Y E T C G K S K N D C D E
E F Q Y C L S K I C R D V Q K T L G L T Q H V Q A C E T T V E L L F D S V I H L G C K P Y L D S Q R A A C R C H Y E E K T D L

Important features:

Signal peptide:

amino acids 1-22

N-myristoylation sites:

amino acids 57-63, 93-99

Phospholipase A2 histidine active site:

amino acids 106-114

Neuraxin and MAP1B proteins repeat proteins Block:

amino acids 109-137

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FIGURE 241

GATTCCGAGCGCCTCCACTGCTGGTCCGTTGGCCAGATCAACTCGCCGCGTGGGCGGCCGTT
CCCTGAGAGTCTGAGCGCTCGCCGCACCCCTTCCGAGCTTCTATTGGCCGTAGCAGACGTCC
GTCTGCCGCTATCTCCGCCCAATACGGAAGCGGCCTAGTCCTCCGGCTCCGACAGCTGGGTG
TCCAGGCCATGGGGCAGCCCTGGGCGGCTGGGAGCACGGACGGGGCGCCCGCGCAGCTGCCTC
TCGTGCTCACCGCGCTGTGGGCCGCGGCCGTGGGCCTGGAGCTGGCTTACGTGCTGGTGCTCG
GTCCCGGGCCGCCGCGCTGGGACCCCTGGCCCGGGCCTTGACAGCTGGCGCTGGCCGCCTTCC
AGCTGCTCAACCTGCTGGGCAACGTGGGGCTCTTCCTGCGCTCGGATCCAGCATCCGTGGCG
TGATGCTGGCCGGCCGCGGTCTGGGCCAGGGCTGGGCTTACTGCTACCAATGCCAAAGCCAGG
TGCCGCCACGCAGCGGACACTGCTCTGCCTGCCGCGTCTGCATCCTGCGTCGGGACCACCACT
GCCGCCTGCTGGGCCGCTGCGTGGGCTTCGGCAACTACCGGCCCTTCCTGTGCCTGCTGCTTC
ATGCCGCCGGCGTCCTGCTCCACGTCTCTGTGCTGCTGGGCCCTGCACTGTGGGCCCTGCTGC
GAGCCACACGCCCCCTCCACATGGCTGCCCTCCTCCTGCTTCCCTGGCTCATGTTGCTCACAG
GCAGAGTGTCTCTGGCACAGTTTGCCTTGGCCTTCGTGACGGACACGTGCGTGGCGGGTGCGC
TGCTGTGCGGGGCTGGGCTGCTCTTCCATGGGATGCTGCTGCTGCGGGGCCAGACCACATGGG
AGTGGGCTCGGGGCCAGCACTCCTATGACCTGGGTCCCTGCCACAACCTGCAGGCAGCCCTGG
GGCCCCGCTGGGCCCTCGTCTGGCTCTGGCCCTTCCTGGCCTCCCCATTGCCTGGGGATGGGA
TCACCTTCCAGACCACAGCAGATGTGGGACACACAGCCTCCTGACTCCAGGAAGAGCCAGAGC
TGTGCAGGGAGGAAGGGGTGAGAGGGGGGCCCCCACACCTAGACTCAGTAAGGAAGTCGGGTT
GGACCTTAACATCTGCATTGGACAACCTCCACCCCTTCCTTGGCCTTGCCCCCTGCCCGCCTACA
CTCCTACGTGTCCAGGGCTTGGGCCGTGACTTAGGCAGAGGAGTGCAGAGCAGGGTCTGGCAG
GGGCTGCTCAGGCCGCCTAGCTGCCCTTTGCCAGGTTAATAAAGCACTGACTTGTTAA

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FIGURE 242

MGQPWAAGSTDGAPAQLPLVLTALWAAVGLLAYVLVLGPGPPPLGPLARALQLALAAFQLL
NLLGNVGLFLRSDPSIRGVMLAGRGLGQGWAYCYQCQSQVPPRSGHCSACRVCILRRDHHCR
LGRCVGFNGYRPFLCLLLHAAGVLLHVSLLGPAALSALLRAHTPLHMAALLLPWLMLLTGRV
SLAQFALAFVTDTCVAGALLCGAGLLFHGMILLRGQTTWEWARGQHSYDLGPCHNLQAALGPR
WALVWLWPFLASPLPGDGITFQTTADVGHAS

Important features:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 51-66, 143-160, 174-191, 198-214

N-myristoylation sites:

amino acids 2-8, 8-14, 30-36, 81-87, 88-94, 90-96, 206-212

Leucine zipper pattern:

amino acids 143-165, 150-172, 157-179, 164-186

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FIGURE 243

CTTGTCTTTGTGTCGGTTGTGATTTTCCTAATCTCTGATTTTCCTTTTCTCTCGGACGCTCTC
CCTCTTCGGACCCATTTTCTCCCGTGCTTCATGCCCTGATAGCCTGGCCCCCTTCCCGGCTTCC
TTCGCTACCGGGGACGCCTCTAGTTTTTCTGAATTTCTGGCTGGCTCCACCCTCCGCGTTCAT
CTTCCTCAAGAGTTCGCCCCCTCTGGGGGCTCCTCTGTGTAATCGTCGCCTTCTCTGGGTATTT
CTGTGAACTCCGTCTCACACCATCCCGCCATCTTCTCTGCCTTGGCCCCCTTTTCTCTGTACAG
CCAGCTCTGTGTCCTTTTCTTCTCCCCCTCTAAAATCGACTCCTCTTCTCCCTGAGAGCCCCA
CCTTTGTGCCCCACTCCTCATTTTCTTCTACGCCTCCCTCTCTCTGCTGGTCCTCTCTCTCCCTG
CAAGGTTCATTCCATCAATTTGTTTGTCTTTTGTAGGGGTGGCATCCCCCTCTGACTACTGCT
CCATCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCTTGAGGATTTCACTTCAATCTTTTCTGGT
TGCGTCTCCACTTGTACTCAGCTTGTTAGGTCCAGGTCCAGTTGTTCTGCATCTGAGGCTGGC
GTGTGCTGTCTTCTCTGATTGGCCTAATCTCCCTCACCCCCGTGAGATCTGTTGTCAGCCTTC
GTTTCTCTTTTCTGTGTCCCAGCTTTTCTGCGGGTCTTGGCACCTTTCTTGGCCACAGATTTT
TGGGTTACAGAGCATGTGTGTCTGAGGCATTGCAGGCAGAAAAGGGTGGCCGACGTGACCTCT
AGCTGGACTGCTGGGCAGGGGAGCTGTCTAGATAAAAATTGGAAAGAAACAGTGACCCAGAGA
CAGGTGGACAAAGAATTCGGGGACTGATGGGAACTGAGCTTGGGATCCAGACTGAAACTGATT
CCAGACTGACCTCTAGCACCCAGGACCCAGACACAGGGGCCATGGGGACCCCAGCATTTGAGACT
TGTGCAGCTGTTCTGCCTTCTAGGGGGCCATCCCCACTCTGCCTCGGGCTGGAGCTCTTTTGTG
CTATGAAGCAACAGCCTCAAGATTCAGAGCTGTTGCTTTCCATAACTGGAAGTGGCTTCTGAT
GAGGAACATGGTGTGTAAGCTGCAAGAGGGCTGCGAGGAGACGCTAGTGTTCAATTGAGACAGG
GACTGCAAGGGGAGTTGTGGGCTTTAAAGGCTGCAGCTCGTCTTACCTGCGCAAAT
CTCCTACCTTGTTTTCCCCACCCGGAGTGTCCATTGCCTCCTACAGTCGCGTCTGCCGGTCTTA
TCTCTGCAACAACCTCACCAATTTGGAGCCTTTTGTGAAACTCAAGGCCAGCACTCCTAAGTC
TATCACATCTGCGTCCTGTAGCTGCCCCGACCTGTGTGGGCGAGCACATGAAGGATTGCCTCCC
AAATTTTGTACCACTAATTCTTGCCCCCTTGGCTGCTTCTACGTGTTACAGTTCCACCTTAAA
ATTTCAAGCAGGGTTTCTCAATACCACCTTCCTCCTCATGGGGTGTGCTCGTGAACATAACCA
GCTTTTAGCAGATTTTCATCATATTGGGAGCATCAAAGTGACTGAGGTCTCAACATCTTAGA
GAAGTCTCAGATTGTTGGTGCAGCATCCTCCAGGCAAGATCCTGCTTGGGGTGTGCTCTTAGG
CCTCCTGTTTGCCTTCAGGGACTTGACCATCTAGCTGCACCCGACAAGCACCCAGACTCTTTCA
CATAACAAATAAAATAGCAGAGTTCCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAA

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FIGURE 244

MGPQHLRLVQLFCLLGAIPTLPRAGALLCYEATASRFRVAFAHNWKWLLMRNMVCKLQEGCEE
TLVFIETGTARGVVGFKGCSSSSSYPAQISYLVSPPGVSIASYSRVCRSYLCNNLTNLEPFVK
LKASTPKSITSASCSCPTCVGEHMKDCLPNFVTTNSCPLAASTCYSSSTLKFQAGFLNTTFLLM
GCAREHNQLLADFHIGSIKVTEVLNILEKSQIVGAASSRQDPAWGVVLGLLFAFRD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation sites:

amino acids 117-121, 183-187

N-myristoylation sites:amino acids 16-22, 25-31, 60-66, 71-77, 81-87, 100-106, 224-230,
235-241, 239-245**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 181-192

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FIGURE 245

GTGGAGTTGGGTGGTGTCTGGGAGCCTCTCCCTGAGGGGACCGCGTCTTCAGGAGCTGGGCCTCCAGTGCGGGCGC
GATGTCAGGCGCGGTGACAGCTCTGTGAGTCCGAGGCCGCGGCCGTGGCGCTGGGCGGCTGCGGGGCCTGACCGG
TCCGCTC**CATG**GTGCCGCCACGACGCCATCGCGGGCAGGAAGGCCAGGGGTGCTGAGTTCCTCACCTCCTTTTAG
ACTGAGATCTGCCAAGTTTTCCGGCATTGCTCTTGAGGATCTCAGAAGGGCTCTTAAGACAAGACTGCAAATGGT
GTGTGTATTTGTCATGAACCGAATGAATTCCCAGAACAGTGGTTTCACCTCAGCGCAGGCGAATGGCTCTTGGGAT
TGTTATTCTTCTGCTTGTTGATGTGATATGGGTTGCTTCCTCTGAACTTACTTCGTATGTTTTTACCCAGTACAA
CAAACCATTCCTTCAGCACCTTTGCAAAAACATCTATGTTTGTGTTTGTACCTTTTGGGCTTTATTATTTGGAAGCC
ATGGAGACAACAGTGTACAAGAGGACTTCGCGGAAAGCATGCTGCTTTTTTGCAGATGCTGAAGGTTACTTTGC
TGCTTGACACAACAGATACAACATGAATAGTTCTTTGAGTGAACCTCTGTATGTGCCTGTGAAATTCCATGATCT
TCCAAGTGAAAAACCTGAGAGCACAAACATTGATACTGAAAAACCCCCAAAAAGTCTCGTGTGAGGTTCAGTAA
TATCATGGAGATTTCGACAGCTTCCGTCAAGTCATGCATTGGAAGCAAAGTTGTCTCGCATGTCATATCCTGTGAA
AGAACAAGAATCCATACTGAAAACCTGTGGGGAAACTTACTGCAACTCAAGTAGCGAAAATTAGCTTTTTTTTTTG
CTTTGTGTGGTTTTTTGGCAAATTTGTCATATCAAGAAGCACTTTCAGACACACAAGTTGCTATAGTTAATATTTT
ATCTTCAACTTCCGGACTTTTTACCTTAATCCTTGCTGCAGTATTTCCAAGTAACAGTGGAGATAGATTTACCCT
TTCTAAACTATTAGCTGTAATTTTAAGCATTGGAGGCGTTGTACTGGTAAACCTGGCAGGGTCTGAAAAACCTGC
TGGAAGAGACACAGTAGGTTCCATTTGGTCTCTTGCTGGAGCCATGCTCTATGCTGTCTATATTGTTATGATTAA
GAGAAAAGTAGATAGAGAAGACAAGTTGGATATTCCAATGTTCTTTGGTTTTGTAGGTTTGTGTTAATCTGCTGCT
CTTATGGCCAGGTTTTCTTTTTACTTCATTATACTGGATTTGAGGACTTCGAGTTTCCCAATAAAGTAGTATTAAT
GTGCATTATCATTAAATGGCCTTATTGGAACAGTACTCTCAGAGTTCCTGTGGTTGTGGGGCTGCTTTCTTACCTC
ATCATTGATAGGCACACTTGCACTAAGCCTTACAATACCTCTGTCCATAATAGCTGACATGTGTATGCAAAGGT
GCAGTTTTCTTGTTATTTTTTGCAGGAGCTATCCCTGTATTTTTTTTCATTTTTTATTGTAACCTCTCCTATGCCA
TTATAATAATTGGGATCCTGTGATGGTGGGAATCAGAAGAATATTTGCTTTTATATGCAGAAAACATCGAATTCA
GAGAGTTCCAGAAGACAGCGAACAGTGTGAGAGTCTCATTTCTATGCACAGTGTTCCTCAGGAGGATGGAGCTAG
T**TAG**CTGTCTGTTGTCTGTAGCCCAGCTTGATAATGGAACATAACAGCGAAGAGACAATCTCTGGCAAGTTTTTG
TAGAAAAATGTTTCAGTGCCTAGTCTGAAAAATAACAGTTTGAGTTCTTTGAAACTCTAAAATATATTTTTCTC
ATACCTGTTTTCTTCATTTTCATAATGAAGCACTTTGCTATGTAGCTGTGTACATATCACTACAGTTATAGGAAG
TTTCAGTCTACAGTCCATCCAAAGGACCAACCTGCCTTACACATCTCAAGGAATTCAGCTGTTGAAATCATTGTA
ACTAATCAAGGAATAAATCCTAATGTTCTGGGACTTTATTTTTACATGTTAAATGCTGGAATATATTATGAAAAT
GTTTTCAAGAAATCACTTAAGTGTTTCATAGACCAGTATTTCTGACAGGTAAAATGCTAAAATAAGCTACCTGTAA
TAAGTGTGGATTATATTTTTTGGGTTTTGTAGAATATTGCAAATTAACCACACAAAAAATGTTTAATTTATGCAAC
AAGCATGTTTGTGCAAATTTTCATGGGACTTTAAAAAGAATAAGTATTTGAGAAAATATCTGTTCACTTACACTA
CATTTACTGTATTATCTTTTATAGCATTAGGTGCCTTGATTTTTAAATCTGTGACAAACCATGGCAAATTTTTTA
AAGGGGAAGTATTATTATAAAATGAAGAAATATGTATTTCTAAAGGCTATATTGCTGTAAACTTAATTGATAAAG
CTCTGTTTAATTTAGAGTTTTGAAGAAATAGTCTCCCTCAATTAAGAAATTTTCATAATGGAATGATTTAAATT
GAAGTGACAAAGAGTATTATTAAAAATACAATGTTTATAAAAAA

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FIGURE 246

MVPPRRHRGAGRPGVLSSSPFRLRS AKFSGIALEDLRRALKTRLQMVCVFVMNRMNSQNSGF
TQRRRMALGIVILLLLVDVIWVASSELTSYVFTQYNKPFFSTFAKTSMFVLYLLGFIIWKPWRQ
QCTRGLRGKHAAFFADAEGYFAACTTDTTMNSSLSEPLYVPVKFHDLPSEKPESTNIDTEKTP
KKS RVRF SNIMEIRQLPSSHALEAKLSRMSYPVKEQESILKTVGKLTATQVAKISFFFCFVWF
LANLSYQEALSDTQVAIVNILSSTSGLFTLILAAVFPSNSGDRFTLSKLLAVILSIGGVVLVN
LAGSEKPAGRDTVGSIWLAGAMLYAVYIVMIKRKVDREDKLDIPMFFGFVGLFNLLLLWPGF
FLLHYTGFEDEFEPNKVVLMCIIINGLIGTVLSEFLWLWGCFLTSSLIGTLALS LTIPLSIIA
DMCMQKVQFSWLFFAGAI PVFFSFFIVTLLCHYNNWDPVMVGIRRI FAFICRKHRIQRPEDS
EQCESLISMHSVSQEDGAS

Important features:**Transmembrane domain:**

amino acids 69-87, 105-118, 237-256, 266-285, 300-316, 332-346,
364-379, 399-419, 453-472

N-glycosylation sites:

amino acids 157-161, 255-259

N-myristoylation sites:

amino acids 14-20, 329-335, 404-410, 407-413, 418-424

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FIGURE 247

CGTCTGTAGAGATATCATGAACTTCAACTTAGCTTTGGTACTTTCTTCCCTGAAGACAGAGGG
CAGAACTCTGAGTTCCAGAACCATTTTCAACTGTATTGGGGACCAATCACTTGACTCTATTCT
TGTCTCTCTGACAGATGACGCTACACTCTCCTCTGAATAATGGACACCATTCTAAAAGTGA
TCCTGCTACTAAAATAATTCAGATGATATATTTTTCCAATTCTACAATCTTGCTTTGTTTTAT
TTAGTTGTTTTCTCTCTCTCTTCCCAGTTTTCCAGAGACTGGAGCTAAACTGGGCTTTCAACA
TCATCATGAAGTTTATCCTCCTCTGGGCCCTCTTGAATCTGACTGTTGCTTTGGCCTTTAATC
CAGATTACACAGTCAGCTCCACTCCCCCTTACTTGGTCTATTTGAAATCTGACTACTTGCCCT
GCGCTGGAGTCCTGATCCACCCGCTTTGGGTGATCACAGCTGCACACTGCAATTTACCAAAGC
TTCGGGTGATATTGGGGGTACAATCCCAGCAGACTCTAATGAAAAGCATCTGCAAGTGATTG
GCTATGAGAAGATGATTCATCATCCACACTTCTCAGTCACTTCTATTGATCATGACATCATGC
TAATCAAGCTGAAAACAGAGGCTGAACTCAATGACTATGTGAAATTAGCCAACCTGCCCTACC
AAACTATCTCTGAAAATACCATGTGCTCTGTCTCTACCTGGAGCTACAATGTGTGTGATATCT
ACAAAGAGCCCGATTCACTGCAAACCTGTGAACATCTCTGTAATCTCCAAGCCTCAGTGTGCGG
ATGCCTATAAAACCTACAACATCACGGAAAATATGCTGTGTGTGGGCATTGTGCCAGGAAGGA
GGCAGCCCTGCAAGGAAGTTTCTGCTGCCCCGGCAATCTGCAATGGGATGCTTCAAGGAATCC
TGTCTTTTGCGGATGGATGTGTTTTGAGAGCCGATGTTGGCATCTATGCCAAAATTTTTTACT
ATATACCCTGGATTGAAAATGTAATCCAAAATAACTTGAGCTGTGGCAGTTGTGGACCATATGA
CACAGCTTGTCCCCATCGTTCACCTTTAGAATTAAATATAAATTAACCTCCTC

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FIGURE 248

MKFILLWALLNLTVALAFNPDYTVSSTPPYLVYLKSDYLPAGVLIHPLWVITAAHCNLPKLR
VILGVTIPADSNEKHLQVIGYEKMIHHPHFSVTSIDHDIMLIKLTAEELNDYVKLANLPYQT
ISENTMCSVSTWSYNVCDIYKEPDSLQTVNISVISKPQCRDAYKTYNITENMLCVGIVPGRRQ
PCKEVSAAPAICNGMLQGILSFADGCVLRADVGIIYAKIFYIIPWIENVIQNN

Important features:**Signal peptide:**

amino acids 1-17

N-glycosylation sites:

amino acids 11-15, 156-160, 173-177

Tyrosine kinase phosphorylation site:

amino acids 108-117

N-myristoylation sites:

amino acids 182-188, 203-209

Amidation site:

amino acids 185-189

Serine proteases, trypsin family, histidine active site:

amino acids 52-58

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FIGURE 249

GCGAGGCGGCCGCTGTCTTCTGCTGCGGCTTCCGCGACCACAAGTACTGCTGCGACGACCCGC
ACAGCTTCTTCCCCTACGAGCACAGCTACATGTGGTGGCTCAGCATTGGCGCTCTCATAGGCC
TGTCCGTAGCAGCAGTGGTTCTTCTCGCCTTCATTGTTACCGCCTGTGTGCTCTGCTACCTGT
TCATCAGCTCTAAGCCCCACACAAAGTTGGACCTGGGCTTGAGCTTACAGACAGCAGGCCCTG
AGGAGGTTTCTCCTGACTGCCAAGGTGTGAACACAGGCATGGCGGCAGAAGTGCCAAAAGTGA
GCCCTCTCCAGCAGAGTTACTCCTGCTTGAACCCGCAGCTGGAGAGCAATGAGGGGCAGGCTG
TGAACTCCAAACGCCTCCTCCATCATTGCTTCATGGCCACAGTGACCACCAGTGACATTCCAG
GCAGCCCTGAGGAAGCCTCTGTACCCAACCCTGACCTATGTGGACCAGTCCCATAAACATTCA
ATAAATGTCTCCATACCATCAA

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FIGURE 250

MWWLSIGALIGLSVAADVLLAFIVTACVLCYLFISSKPHTKLDLGLSLQTAGPEEVSPDCQGV
NTGMAAEVPKVSPLQQSYSCLN PQLESNEGQAVNSKRL LHCFMATVTTSDIPGSPEEASVPN
PDL CGPVP

Important features:

Signal peptide:

Amino acids 1-26

N-myristoylation sites:

Amino acids 7-13, 11-17, 62-68, 93-99

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FIGURE 251

GTGGTTTGGATTGAGCCGGGCCCCGGCCGGGGCGCCGAGTCGGAGGGGGTGGCAGTGAGCGGCG
GCAGAGGGCTACGGGGCTCGGTTTGGCTGACTGGGGAGTCGGCAGGCGGCAGGAACCATGCGAG
GCCAGCGGAGCCTGCTGCTGGGCCCCGGCCCGCCTCTGCCTCCGCCTCCTTCTGCTGCTGGGTT
ACAGGCGCCGCTGTCCACCTCTACTCCGGGGTCTAGTACAGCGCTGGCGCTACGGCAAGGTCT
GCCTGCGCTCCCTGCTCTACAACTCCTTTGGGGGCGAGTGACACCGCTGTTGATGCTGCCTTTG
AGCCTGTCTACTGGCTGGTAGACAACGTGATCCGCTGGTTTGGAGTGGTGTTCGTGGTCCTGG
TGATCGTGCTGACAGGCTCCATTGTAGCTATCGCCTACCTGTGTGTCTGCTCTCATCCTCC
GAACCTACTCAGTGCCACGACTCTGCTGGCATTCTTCTATAGCCACTGGAATCTGATCCTGA
TTGTCTTCCACTACTACCAGGCCATCACCCTCCGCCTGGGTACCCACCCCAGGGCAGGAATG
ATATCGCCACCGTCTCCATCTGTAAGAAGTGCATTTACCCCAAGCCAGCCCGAACACACCACT
GCAGCATCTGCAACAGGTGTGTGCTGAAGATGGATCACCCTGCCCTGGCTAAACAATTGTG
TGGGCCACTATAACCATCGGTACTTCTTCTCTTTCTGCTTTTTTCATGACTCTGGGCTGTGTCT
ACTGCAGCTATGGAAGTTGGGACCTTTTCCGGGAGGCTTATGCTGCCATTGAGACTTATCACC
AGACCCCAACCAACCACTTCTCCTTTTCGAGAAAGGATGACTCACAAGAGTCTTGTCTACCTCT
GGTTCCTGTGCAGTTCTGTGGCACTTGCCCTGGGTGCCCTAACTGTATGGCATGCTGTTCTCA
TCAGTCGAGGTGAGACTAGCATCGAAAGGCACATCAACAAGAAGGAGAGACGTCGGCTACAGG
CCAAGGGCAGAGTATTTAGGAATCCTTACAACCTACGGCTGCTTGGACAACCTGGAAGGTATTCC
TGGGTGTGGATACAGGAAGGCACTGGCTTACTCGGGTGCTCTTACCTTCTAGTCACTTGCCCC
ATGGGAATGGAATGAGCTGGGAGCCCCCTCCCTGGGTGACTGCTCACTCAGCCTCTGTGATGG
CAGTGTAAGCTGGACTGTGTCAGCCACGACTCGAGCACTCATTCTGCTCCCTATGTTATTTCA
AGGGCCTCCAAGGGCAGCTTTTCTCAGAATCCTTGATCAAAAAGAGCCAGTGGGCCTGCCTTA
GGGTACCATGCAGGACAATTCAAGGACCAGCCTTTTACCCTGCAGAAGAAAGACACAATGT
GGAGAAATCTTAGGACTGACATCCCTTTACTCAGGCAAACAGAAGTTCCAACCCCACTAGG
GGTCAGGCAGCTAGCTACCTACCTTGCCCAGTGCTGACCCGGACCTCCTCCAGGATACAGCAC
TGGAGTTGGCCACCACCTCTTCTACTTGCTGTCTGAAAAAACACCTGACTAGTACAGCTGAGA
TCTTGGCTTCTCAACAGGGCAAAGATAACCAGGCCTGCTGCTGAGGTCACTGCCACTTCTCACA
TGCTGCTTAAGGGAGCACAAATAAAGGTATTGATTTTTTAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

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FIGURE 252

MRGQRSLLLGPARGCLRLLLLLGYRRRCPLLRLVQRWRYGKVCLRSLLYNSFGGSDTAVDA
AFEPVYWLVDNVIRWFGVVFVVLVIVLTGSIVAIAIAYLCVLPILIRTVSPRLCWHFFYSHWNL
ILIVFHYYQAITTPPGYPPQGRNDIATVSICKKCIYPKPARTHHCSICNRCVLKMDHHC PWLN
NCVGHYNHRYFFSFCFFMTLGCVCYCSYGSWDLFREAYAAIETYHQTPPTFSFRERMTHKSLV
YLWFLCSSVALALGALTVWHAVLISRGETS IERHINKKERRRLQAKGRVFRNPYNYGCLDNWK
VFLGVDTGRLHLTRVLLPSSHLPHGNGMSWEPPPWVTAHSASVMAV

Important features:**Transmembrane domain:**

amino acids 88-100, 202-216, 254-274

N-myristoylation sites:

amino acids 55-61, 56-62, 92-98, 210-216, 309-315, 319-325, 340-346

Prokaryotic membrane lipoprotein lipid attachment site:

amino acids 201-212

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FIGURE 253

GATCAAGCGCCTTCCCTTCCCTTCTCTCTCCCTACTGGCCTTTGCCCTAAGCCAAGACCTGGCCATCAGCCTTGGC
TGCAGGGGGCCTGCAGAGCCAGCTGCACTTTTTTTCAGGTATGGGGGAGGGCCAGGCACCATGAAGCCAGTGTGGGTCT
GCCACCCTTCTGTGGATGCTACTGCTGGTGGCCAGGCTGGGGGGCCGCCCGGAAGGGGTCCCCAGAAGAGGCCTCC
TTCTACTATGGAACCTTCCCTCTTGGCTTCTCTCTGGGGCGTGGGCAGTTCTGCCTACCAGACGGAGGGGCGCTGG
GACCAGGACGGGAAAGGGCCTAGCATCTGGGACGTCTTCACACACAGTGGGAAGGGGAAAGTGCTTGGGAATGAG
ACGGCAGATGTAGCCTGTGACGGCTACTACAAGGTCCAGGAGGACATCATCTGCTGAGGGAACTGCACGTCAAC
CACTACCGATTCTCCCTGTCTTGGCCCCGGCTCCTGCCCACAGGCATCCGAGCCGAGCAGGTGAACAAGAAGGGA
ATCGAATTCTACAGTGATCTTATCGATGCCCTTCTGAGCAGCAACATCACTCCCATCGTGACCTTGCACCACTGG
GATCTGCCACAGCTGCTCCAGGTCAAATACGGTGGGTGGCAGAATGTGAGCATGGCCAACTACTTCAGAGACTAC
GCCAACCTGTGCTTTGAGGCCTTTGGGGACCGTGTGAAGCACTGGATCACGTTCACTGATCCTCGGGCAATGGCA
GAAAAAGGCTATGAGACGGGCCACCATGCGCCGGGCCTGAAGCTCCGCGGCACCGGCCTGTACAAGGCAGCACAC
CACATCATTAAGGCCCACGCCAAAACCTGGCATTCTTATAACACCACGTGGCGCAGCAAGCAGCAAGGTCTGGTG
GGAAATTTCACTGAACTGTGACTGGGGGGAACCTGTGGACATTAGTAACCCCAAGGACCTAGAGGCTGCCGAGAGA
TACCTACAGTTCTGTCTGGGCTGGTTTGCCAACCCCATTTATGCCGGTGACTACCCCCAAGTCATGAAGGACTAC
ATTGGAAGAAAGAGTGCAGAGCAAGGCCTGGAGATGTGAGGTTACCGGTGTTCTCACTCCAGGAGAAGAGCTAC
ATTAAGGCACATCCGATTTCTTGGGATTAGGTCATTTTACTACTCGGTACATCACGGAAAGGAACTACCCCTCC
CGCCAGGGGGCCAGCTACCAGAACGATCGTGACTTGATAGAGCTGGTGTACCCAACTGGCCAGATCTGGGGTCT
AAATGGCTATATTCTGTGCCATGGGGATTTAGGAGGCTCCTTAACCTTTGCTCAGACTCAATACGGTGATCCTCCC
ATATATGTGATGGAAAATGGAGCATCTCAAAAATTCCACTGTACTCAATTATGTGATGAGTGGAGAATTCAATAC
CTTAAAGGATACATAAATGAAATGCTAAAAGCTATAAAAGATGGTGCTAATATAAAGGGGTATACTTCCCTGGTCT
CTGTTGGATAAGTTTGAATGGGAGAAAGGATACTCAGATAGATATGGATTCTACTATGTTGAATTTAACGACAGA
AATAAGCCTCGCTATCCAAAGGCTTCAGTTCAATATTACAAGAAGATTATCATTGCCAATGGGTTTTCCAATCCA
AGAGAGGTGGAAAGTTGGTACCTCAAAGCTTTGGAAACTTGCTCTATCAACAATCAGATGCTTGCTGCAGAGCCT
TTGCTAAGTCACATGCAAATGGTTACGGAGATCGTGGTACCCACTGTCTGCTCCCTCTGTGTCCTCATCACTGCT
GTTCTACTAATGCTCCTCCTGAGGAGGCAGAGCTTGAGACAGGATTATCAATTTTGGAGCTTCATAAGAGAATCTT
CAGGATCTTCCTCCCTTTTTCTGCTTTGAGGGTTTCCATACATTGCTGTTTTCAGGTTCTACAATAATTACCTTTT
TTTCTCTTTCTCTTTTTGGCTTGTGCTGGGATTTAAGAATTAGAAAAATAAAAAATAAGCAGAAATTA

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FIGURE 254

MKPVWVATLLWMLLLVPRLGAARKGSPEEASFYYGTFFPLGFSWVGSSAYQTEGAWDQDGKGPSIWDVFTHSGKG
 KVLGNETADVACDGYKQVEDIILLRELHVNHYRFSLSWPRLPTGIRAEQVNKKGIEFYSDLIDALLSSNITPI
 VTLHHWDLPLQLLOVKYGGWQNVSMANYFRDYANLCFEAFGDRVKHWITFSDPRAMAEGYETGHHAPGLKLRGTG
 LYKAAHHIIKAHAKTWHSYNTTWRSKQQGLVGISLNCWGEVVDISNPKDLEAAERYLQFCLGWFANPIYAGDYP
 QVMKDYIGRKSAEQGLEMSRLPVFSLQEKSYIKGTSDFLGLGHFTTRYITERNYPSRQGPSYQNDRLIELVDPN
 WPDLGSKWLYSVPWGFRRLLNFAQTQYGDPIIYVMENGASQKFHCTQLCDEWRIQYLKGYINEMLKAIKDGANIK
 GYTSWSLLDKFEWEKGYSDRYGFYYVEFNDNRNPKPRYPKASVQYYKKIIANGFPNPREVESWYLKALETCSINNQ
 MLAAEPLLSHMQMVTEIVVPTVCSLCVLITAVLLMLLLRRQS

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 541-558

N-glycosylation sites:

amino acids 80-84, 171-175, 245-249

Glycosaminoglycan attachment site:

amino acids 72-76

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

amino acids 23-27, 564-568

Tyrosine kinase phosphorylation sites:

amino acids 203-211, 347-355, 460-468, 507-514

N-myristoylation sites:

amino acids 44-50, 79-85, 167-173, 225-231, 257-263, 315-321

Amidation site:

amino acids 307-311

Glycosyl hydrolases family 1 active site:

amino acids 407-416

Glycosyl hydrolases family 1 N-terminal signature:

amino acids 41-56

Motif name Glycosyl hydrolases family:

amino acids 37- 67

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FIGURE 255

CGCGAAGATGCGAAAGGTGGTTTTGATCACCGGGGCTAGCAGTGGCATTGGCCTGGCCCTCTG
CAAGCGGCTGCTGGCGGAAGATGATGAGCTTCATCTGTGTTTGGCGTGCAGGAACATGAGCAA
GGCAGAAGCTGTCTGTGCTGCTCTGCTGGCCTCTCACCCCCTGCTGAGGTCACCATTGTCCA
GGTGGATGTCAGCAACCTGCAGTCGGTCTTCCGGGGCCTCCAAGGAACCTTAAGCAAAGGTTTCA
GAGATTAGACTGTATATATCTAAATGCTGGGATCATGCCTAATCCACAACCTAAATATCAAAGC
ACTTTTCTTTGGCCTCTTTTCAAGAAAAGTGATTTCATATGTTCTCCACAGCTGAAGGCCTGCT
GACCCAGGGTGATAAGATCACTGCTGATGGACTTCAGGAGGTGTTTGAGACCAATGTCTTTGG
CCATTTTATCCTGATTCGGGAACTGGAGCCTCTCCTCTGTACAGTGACAATCCATCTCAGCT
CATCTGGACATCATCTCGCAGTGCAAGGAAATCTAATTTTCAGCCTCGAGGACTTCCAGCACAG
CAAAGGCAAGGAACCCTACAGCTCTTCCAAATATGCCACTGACCTTTTGAGTGTGGCTTTGAA
CAGGAACCTTCAACCAGCAGGGTCTCTATTCCAATGTGGCCTGTCCAGGTACAGCATTGACCAA
TTTGACATATGGAATTCTGCCTCCGTTTATATGGACGCTGTTGATGCCGGCAATATTGCTACT
TCGCTTTTTTTGCAAATGCATTCACTTTGACACCATATAATGGAACAGAAGCTCTGGTATGGCT
TTTCCACCAAAAGCCTGAATCTCTCAATCCTCTGATCAAATATCTGAGTGCCACCACTGGCTT
TGGAAGAAATTATATTATGACCCAGAAGATGGACCTAGATGAAGACACTGCTGAAAAATTTTA
TCAAAGTTACTGGAAGTGGAAAAGCACATTAGGGTCACTATTCAAAAAACAGATAATCAGGC
CAGGCTCAGTGGCTCATGCCTATAATTCCAGCACTTTGGGAGGCCAAGGCAGAAGGATCACTT
GAGACCAGGAGTTCAAGACCAGCCTGAGAAACATAGTGAGCCCTTGTCTCTACAAAAAGAAAT
AAAAATAATAGCTGGGTGTGGTGGCATGCGCATGTAGTCCCAGCTACTCAGAAGGATGAGGTG
GGAGGATCTCTTGAGGCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTGTGCCACTGCACTCC
AGCCTGGGTGACAGCGAGACCCTGTCTCAAATATGTATATATTTAATATATATATAAAACCA
GAGCTGACAATGACACTCTGGAACATTGCATACCTTCTGTACATTCTGGGGTACATGGATTTT
TACTGAGTTGGATAATATGCATTTGTAATAAACTATGAACTATGAA

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FIGURE 256

MRKVVLITGASSGIGLALCKRLLAEDDELHLCLACRNMSKAEAVCAALLASHPTAEVTIVQVD
VSNLQSVFRASKELKQRFQRLDCIYLNAGIMPNPQLNIKALFFGLFSRKVIHMFSTAEGLLTQ
GDKITADGLQEVFETNVFGHFILIRELEPLLCHSDNPSQLIWTSSRSARKSNFSLEDFQHSGK
KEPYSSSKYATDLLSVALNRNFNQQGLYSNVACPGTALTNLTYGILPPFIWTLLMPAILLLRF
FANAFTLTPYNGTEALVWLFHQKPESLNPLIKYLSATTGFGRNYIMTQKMDLDEDTAEKFYQK
LLELEKHIRVTIQKTDNQARLSGSCL

Important features:**Transmembrane domain:**

amino acids 234-254

N-glycosylation sites:

amino acids 37-41, 178-182, 229-233, 263-267

Glycosaminoglycan attachment site:

amino acids 12-16

N-myristoylation sites:

amino acids 9-15, 13-19, 15-21, 215-221, 224-230

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FIGURE 257

CGGACGCGTGGGGCCGTATGCGCGGCTCTGTGGAGTGCACCTGGGGTTGGGGGCACTGTGCCC
CCAGCCCCCTGCTCCTTTGGACTCTACTTCTGTTTGCAGCCCCATTTGGCCTGCTGGGGGAGA
AGACCCGCCAGGTGTCTCTGGAGGTCATCCCTAACTGGCTGGGCCCCCTGCAGAACCTGCTTC
ATATACGGGCAGTGGGCACCAATTCCACACTGCACTATGTGTGGAGCAGCCTGGGGCCTCTGG
CAGTGGTAATGGTGGCCACCAACACCCCCACAGCACCTTGAGCATCAACTGGAGCCTCCTGC
TATCCCCTGAGCCCGATGGGGGCCTGATGGTGCTCCCTAAGGACAGCATTTCAGTTTTCTTCTG
CCCTTGTTTTTACCAGGCTGCTTGAGTTTGACAGCACCAACGTGTCCGATACGGCAGCAAAGC
CTTTGGGAAGACCATATCCTCCATACTCCTTGGCCGATTTCTCTTGGAACAACATCACTGATT
CATTGGATCCTGCCACCCTGAGTGCCACATTTCAAGGCCACCCCATGAACGACCCTACCAGGA
CTTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGCCTTTTCCAGGTCCAGCCGACCAGCCC
AACCCCTCGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGCCCTGATTGGAGCCT
CTCCCCGGGGAAACCGTTCCCTGTTTGGGCTGGAGGTAGCCACATTGGGCCAGGGCCCTGACT
GCCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCCGTCTTCCAGTTGG
ACCAGCTACTGTGGGGCTCCCTCCCATCAGGCTTTGCACAGTGGCGACCAGTGGCTTACTCCC
AGAAGCCGGGGGGCCGAGAATCAGCCCTGCCCTGCCAAGCTTCCCCTCTTCATCCTGCCTTAG
CATACTCTCTTCCCCAGTCACCCATTGTCCGAGCCTTCTTTGGGTCCCAGAATAACTTCTGTG
CCTTCAATCTGACGTTTCGGGGCTTCCACAGGCCCTGGCTATTGGGACCAACACTACCTCAGCT
GGTCGATGCTCCTGGGTGTGGGCTTCCCTCCAGTGGACGGCTTGTCCCCACTAGTCCTGGGCA
TCATGGCAGTGGCCCTGGGTGCCCCAGGGCTCATGCTGCTAGGGGGCGGCTTGGTTCTGCTGC
TGCACCACAAGAAGTACTCAGAGTACCAGTCCATAAATTAAGGCCCGCTCTCTGGAGGGAAGG
ACATTACTGAACCTGTCTTGCTGTGCCTCGAAACTCTGGAGGTTGGAGCATCAAGTTCCAGCC
GGCCCCTTCACTCCCCCATCTTGCTTTTCTGTGGAACCTCAGAGGCCAGCCTCGACTTCCTGG
AGACCCCCAGGTGGGGCTTCCTTCATACTTTGTTGGGGGACTTTGGAGGCGGGCAGGGGACAG
GGCTATTGATAAGGTCCCCTTGGTGTTGCCTTCTTGCATCTCCACACATTTCCCTTGGATGGG
ACTTGCAGGCCTAAATGAGAGGCATTCTGACTGGTTGGCTGCCCTGGAAGGCAAGAAAATAGA
TTTATTTTTTTTTCACAGGGGAAAAAAAAAAAA

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FIGURE 258

MRGSVECTWGWGHCAPSPLLLWTLTLLFAAPFGLLGKTRQVSLEVIPNWLGPQNLLHIRAVG
TNSTLHYVWSSSLGPLAVVMVATNTPHSTLSINWSLLLSPEPDGGLMVLPKDSIQFSSALVFTR
LLEFDSTNVSDTAAKPLGRPYPPYSLADESWNNITDSLDPATLSATFQGHMNDPTRTFANGS
LAFRVQAFSRSSRPAQPPRLHTADTCQLEVALIGASPRGNRSLFGLEVATLGQGPDCPSMQE
QHSIDDEYAPAVFQLDQLLWGSLSGFAQWRPVAYSQKPGGRESALPCQASPLHPALAYSLPQ
SPIVRAFFGSQNNFCAFNLTFGASTGPGYWDQHYLSWSMLLGVGFPPVDGLSPLVLGIMAVAL
GAPGLMLLGGGLVLLLHHKKYSEYQSIN

Important features:**Signal peptide:**

amino acids 1-35

Transmembrane domain:

amino acids 365-386

N-glycosylation sites:

amino acids 65-69, 95-99, 134-138, 159-163, 187-191, 230-234, 333-337

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 397-401

N-myristoylation sites:

amino acids 3-9, 63-69, 235-241, 273-279, 292-298, 324-330

Leucine zipper pattern:

amino acids 371-393

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FIGURE 259

CAGGCGGGCCCCGCGCGGCAGGGCCCTGGACCCGCGCGGCTCCCGGGGATGGTGAGCAAGGCGCTGCTGCGCCT
CGTGTCTGCCGTCAACCGCAGGAGGATGAAGCTGCTGCTGGGCATCGCCTTGCTGGCCTACGTCGCCTCTGTTTG
GGGCAACTTCGTTAATATGAGGTCTATCCAGGAAAATGGTGAAGTAAAAATTGAAAGCAAGATTGAAGAGATGGT
TGAACCACTAAGAGAGAAAAATCAGAGATTTAGAAAAAGCTTTACCCAGAAATACCCACCAGTAAAGTTTTTATC
AGAAAAGGATCGGAAAAAGATTTTGATAACAGGAGGCGCAGGGTTCGTGGGCTCCCATCTAAGTACAACTCAT
GATGGACGGCCACGAGGTGACCGTGGTGGACAATTTCTTCACGGGCAGGAAGAGAAACGTGGAGCACTGGATCGG
ACATGAGAACTTCGAGTTGATTAACCACGACGTGGTGGAGCCCCTCTACATCGAGGTTGACCAGATATACCATCT
GGCATCTCCAGCCTCCCCTCCAACTACATGTATAATCCTATCAAGACATTAAAGACCAATACGATTGGGACATT
AAACATGTTGGGGCTGGCAAAACGAGTCGGTGCCCGTCTGCTCCTGGCCTCCACATCGGAGGTGTATGGAGATCC
TGAAGTCCACCCTCAAAGTGAGGATTACTGGGGCCACGTGAATCCAATAGGACCTCGGGCCTGCTACGATGAAGG
CAAACGTGTTGCAGAGACCATGTGCTATGCCTACATGAAGCAGGAAGGCGTGGAAGTGCAGTGGCCAGAATCTT
CAACACCTTTGGGCCACGCATGCACATGAACGATGGGCGAGTAGTCAGCAACTTCATCCTGCAGGCGCTCCAGGG
GGAGCCACTCACGGTATACGGATCCGGGTCTCAGACAAGGGCGTTCCAGTACGTCAGCGATCTAGTGAATGGCCT
CGTGGCTCTCATGAACAGCAACGTCAGCAGCCCGGTCAACCTGGGGAACCCAGAAGAACACACAATCCTAGAATT
TGCTCAGTTAATTAAAAACCTTGTTGGTAGCGGAAGTGAATTCAGTTTCTCTCCGAAGCCCAGGATGACCCACA
GAAAAGAAAACCAGACATCAAAAAAGCAAAGCTGATGCTGGGGTGGGAGCCCGTGGTCCCGCTGGAGGAAGGTTT
AAACAAAGCAATTCATACTTCCGTAAAGAACTCGAGTACCAGGCAAATAATCAGTACATCCCCAAACCAAAGCC
TGCCAGAATAAAGAAAGGACGGACTCGCCACAGCTTGAACTCCTCACTTTTAGGACACAAGACTACCATTGTACAC
TTGATGGGATGTATTTTTGGCTTTTTTTTTGTTGTCGTTTTAAAGAAAGACTTTAACAGGTGTCATGAAGAACAAAC
TGGAATTTTCACTTCTGAAGCTTGCTTTAATGAAATGGATGTGCCTAAAAGCTCCCCTCAAAAACTGCAGATTTTG
CCTTGCACTTTTTGAATCTCTCTTTTTATGTAAATAGCGTAGATGCATCTCTGCGTATTTTCAAGTTTTTTTAT
CTTGCTGTGAGAGCATATGTTGTGACTGTCGTTGACAGTTTTATTACTGGTTTCTTTGTGAAGCTGAAAAGGAA
CATTAAGCGGGACAAAAAATGCCGATTTTATTTATAAAAGTGGGTACTTAATAAATGAGTCGTTATACTATGCAT
AAAGAAAAATCCTAGCAGTATTGTCAGGTGGTGGTGCGCCGGCATTGATTTTAGGGCAGATAAAAGAATTCTGTG
TGAGAGCTTTATGTTTCTCTTTTAATTCAGAGTTTTTCCAAGGTCTACTTTTGAGTTGCAAACCTGACTTTGAAA
TATTCCTGTTGGTCATGATCAAGGATATTTGAAATCACTACTGTGTTTTGCTGCGTATCTGGGGCGGGGCGAGGT
TGGGGGGCACAAAGTTAACATATTCTTGGTTAACCATGGTTAAATATGCTATTTTAATAAAATATTGAAACTCA

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FIGURE 260

MVSKALLRLVSAVNRRRMKLLLGIALLAYVASVWGNFVNMRSIQENGELKIESKIEEMVEPLR
EKIRDLEKSFTQKYPPVKFLSEKDRKRILITGGAGFVGSHLTDKLMMDGHEVTVVDNFFTGRK
RNVEHWIGHENFELINHADVVEPLYIEVDQIYHLASPPNYMYNPIKTLKTNLTIGTLNMLGL
AKRVGARLLLASTSEVYGDPEVHPQSEDYWGHVNPIGPRACYDEGKRVAETMCYAYMKQEGVE
VRVARIFNTFGPRMHMNDGRVVSFILQALQGEPLTVYSGSQTRAFQYVSDLVNLGLVALMNS
NVSSPVNLGNPEEHTILEFAQLIKNLVSGSGSEIQFLSEAQDDPQKRKPDIKKAKLMLGWEPPV
PLEEGLNKAIHYFRKELEYQANNQYIPKPKPARIKKGRTRHS

Important features:**Signal peptide:**

amino acids 1-32

N-glycosylation site:

amino acids 316-320

Tyrosine kinase phosphorylation site:

amino acids 235-244

N-myristoylation sites:

amino acids 35-41, 101-107, 383-389

Amidation sites:

amino acids 123-127, 233-237

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FIGURE 261

GCGTGGTGGGGGGCGTGGGGAAATCGGGTTGCCCCAGCCGTTACTGGTCCGCGCAGTCAGGG
CATCCTCCGCATCCTCCACATCCTTCCATGGCTCTGAAGAATAAATTTCAGTTGTTTATGGATC
TTGGGTCTGTGTTTGGTAGCCACTACATCTTCCAAAATCCCATCCATCACTGACCCACACTTT
ATAGACAACTGCATAGAAGCCCACAACGAATGGCGTGGCAAAGTCAACCCTCCCGCGGGCCGAC
ATGAAATACATGATTTGGGATAAAGGTTTAGCAAAGATGGCTAAAGCATGGGCAAACCAGTGC
AAATTTGAACATAATGACTGTTTGGATAAATCATATAAATGCTATGCAGCTTTTGAATATGTT
GGAGAAAATATCTGGTTAGGTGGAATAAAGTCATTACACCAAGACATGCCATTACGGCTTGG
TATAATGAAACCCAATTTTATGATTTTGTAGTCTATCATGCTCCAGAGTCTGTGGCCATTAT
ACACAGTTAGTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTCCTAACCTT
GGGGGAGCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAATATG
CCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTAAAGAAC
CTCTGCAGGACTCCACAACCTTATTATACCTAACCAAAATCCATTTCTGAAGCCAACGGGGAGA
GCACCTCAGCAGACAGCCTTTAATCCATTCAGCTTAGGTTTTCTTCTTCTGAGAATCTTTTAA
TGTCATTTATATACAAAAGAAATTCTCAAATGTTAAAATAAAGGAATAGTTTATTGCTTAATA

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FIGURE 262

MALKNKFSCWLWILGLCLVATTSSKIPSITDPHFIDNCIEAHNEWRGKVNPPAADMKYMIWDKG
LAKMAKAWANQCKFEHNDCLDKSYKCYAAFEYVGENIWLGGIKSFTPRHAITAWYNETQFYDF
DSLSCSRVCGHYTQLVWANSFYVGCAMCPNLGGASTAIFVCNYGPAGNFANMPPYARGESC
SLCSKEEKCVKNLCRTPQLIIPNQNPFLKPTGRAPQQTAFNPFSLGFLLLRIF

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation site:

amino acids 119-123

N-myristoylation sites:

amino acids 103-109, 150-156, 160-166, 161-167, 175-181

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1:

amino acids 136-156

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2:

amino acids 166-178

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FIGURE 263

CGCCCTCCGACCCGCCCCGCGGCGCATTGTGGGATCTGTCGGCTTGTCAGGTGGTGGAGGAAA
AGGCGCTCCGTCATGGGGATCCAGACGAGCCCCGTCTGCTGGCCTCCCTGGGGGTGGGGCTG
GTCACCTCTGCTCGGCCTGGCTGTGGGCTCCTACTTGTTTCGGAGGTCCCGCCGGCCTCAGGTC
ACTCTCCTGGACCCCAATGAAAAGTACCTGCTACGACTGCTAGACAAGACGACTGTGAGCCAC
AACACCAAGAGGTTCCGCTTTGCCCTGCCACCGCCCCACCACACTCTGGGGCTGCCTGTGGGC
AAACATATCTACCTCTCCACCCGAATTGATGGCAGCCTGGTCATCAGGCCATACACTCCTGTC
ACCAGTGATGAGGATCAAGGCTATGTGGATCTTGTCATCAAGGTCTACCTGAAGGGTGTGCAC
CCCAAATTTCTGAGGGAGGGAAGATGTCTCAGTACCTGGATAGCCTGAAGGTGGGGATGTG
GTGGAGTTTCGGGGGCCAAGCGGGTTGCTCACTTACACTGGAAAAGGGCATTTTAACATTTCAG
CCCAACAAGAAATCTCCACCAGAACCCCGAGTGGCGAAGAACTGGGAATGATTGCCGGCGGG
ACAGGAATCACCCCAATGCTACAGCTGATCCGGGCCATCCTGAAAGTCCCTGAAGATCCAACC
CAGTGCTTTCTGCTTTTTGCCAACCAGACAGAAAAGGATATCATCTTGCGGGAGGACTTAGAG
GAACTGCAGGCCCCGCTATCCCAATCGCTTTAAGCTCTGGTTCACCTCTGGATCATCCCCAAAA
GATTGGGCCTACAGCAAGGGCTTTGTGACTGCCGACATGATCCGGGAACACCTGCCCGCTCCA
GGGGATGATGTGCTGGTACTGCTTTGTGGGCCACCCCAATGGTGCAGCTGGCCTGCCATCCC
AACTTGGACAACTGGGCTACTCACAAAAGATGCGATTACCTACTTGAGCATCCTCCAGCTTC
CCTGGTGCTGTTTCGCTGCAGTTGTTCCCCATCAGTACTCAAGCACTATAAGCCTTAGATTCTT
TTCCTCAGAGTTTCAGGTTTTTTTCAGTTACATCTAGAGCTGAAATCTGGATAGTACCTGCAGG
AACAATATTCCTGTAGCCATGGAAGAGGGCAAGGCTCAGTCACTCCTTGGATGGCCTCCTAAA
TCTCCCCGTGGCAACAGGTCCAGGAGAGGCCCATGGAGCAGTCTCTTCATGGAGTAAGAAGG
AAGGGAGCATGTACGCTTGGTCCAAGATTGGCTAGTTCCTTGATAGCATCTTACTCTCACCTT
CTTTGTGTCTGTGATGAAAGGAACAGTCTGTGCAATGGGTTTTACTTAACTTCACTGTTCAA
CCTATGAGCAAATCTGTATGTGTGAGTATAAGTTGAGCATAGCATACTTCCAGAGGTGGTNTT
ATGGAGATGGCAAGAAAGGAGGAAATGATTCTTCAGATNTCAAAGGAGTCTGAAATATCATA
TTTCTGTGTGTGTCTCTCTCAGCCCCCTGCCAGGCTAGAGGGAAACAGCTACTGATAATCGAA
AACTGCTGTTTGTGGCANGAACCCCTGGCTGTGCAAATAAATGGGGCTGAGGCCCTGTGTGA
TATTGAAGA

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FIGURE 264

MGIQTSPVLLASLGVLVTLLGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTR
FRFALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQGYVDLVIKVYLKGVHPKFP
EGGKMSQYLDLKVGDVVEFRGPSGLLTGTGKGHFNIQPNKSPPEPRVAKKLGMIAGGTGIT
PMLQLIRAILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFLWFTLDHPPKDWAY
SKGFVTADMIREHLPAPGDDVLVLLCGPPPMVQLACHPNLDKLGYSQKMRFTY

Important features:**Signal peptide:**

amino acids 1-26

N-glycosylation site:

amino acids 214-218

N-myristoylation sites:

amino acids 22-28, 76-82, 128-134, 180-186

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FIGURE 265

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAGA
ACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTATAG
AATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTCGGT
TCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGGCACGATGTTGGGGGCCCCGCCTCAGG
CTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCC
TCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC
AGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTAC
AGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGA
AGATACCTCTGCATGGATTTTCAGAGGCAACATTTTTGGATCACACTATTTTCGACCCGGAGAAC
TGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCAC
TTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTAC
TCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGG
CGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGG
GCCCCGATGACCCCGGCCCGGCCTCCTGTTACAGGAGCTCCCGAGCGCCGAGGACAACAGC
CCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGA
ACGGGCCCCGGAAGGCTGCCGCCCCCTTCGCCAAGTTCATCTAGGGTTCGCTGG

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FIGURE 266

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARN SYHLQIHKN GHVDG
APHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI FGSHYFDPENCRFQHQTLENGYDV
YHSPQYHFLVSLGRAKRAFLPGMNPPPY SQFLSRRNEIPLIHFNTPIPRRHTRSAEDDSERDP
LNVLKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFAKFI

Important features:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

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FIGURE 267

GGCTGAGGGGAGGCCCGAGCCTTTCTGGGGCCTGGGGGATCCTCTTGCACTGGTGGGTGGAGAGAAGCGCCTGC
AGCCAACCAGGGTCAGGCTGTGCTCACAGTTTCCTCTGGCGGCATGTAAAGGCTCCACAAAGGAGTTGGGAGTTC
AAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCCCAAGCCCTGGACCTGCCGAGCGTGGCACTGAGGCAGCGG
CTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCTCTG
CCGGAGCCCTCTGTGGAGGCAGAGCCAGTGGAGCCCAGTGAAGCATGTGAGGAGCCGCCCCGG
CAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATGTGAGGAGCCGCCCCGG
AGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTACAAAGAATAACCACCATTTTGCAAGGACCATGAGG
CCACTGTGCGTGACATGCTGGTGGCTCGGACTGCTGGCTGCCATGGGAGCTGTTGCAGGCCAGGAGGACGGTTTTT
GAGGGCACTGAGGAGGGCTCGCCAAGAGAGTTCAATTTACCTAAACAGGTACAAGCGGGCGGGCGAGTCCCAGGAC
AAGTGCACCTACACCTTCATTGTGCCCCAGCAGCGGGTACGGGTGCCATCTGCGTCAACTCCAAGGAGCCTGAG
GTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCTGCTCAAGCAGAAGCGGCAG
ATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTGTGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGC
CGCAACATGAACTCGCGGGTCACGCAGCTCTACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCG
TTGGAGCTCTCCAGCTGGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAG
GACCTGGAGCACAAGTACCAGCACCTGGCCCACTGGCCCACAACCAATCAGAGATCATCGCGCAGCTTGAGGAG
CACTGCCAGAGGGTGGCCTCGGCCAGGCCCCGTCCCCAGCCACCCCCGCTGCCCCGCCCCGGGTCTACCAACCA
CCCACCTACAACCGCATCATCAACCAGATCTCTACCAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCA
CCCCCTCTGCCCCACTATGCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTGGGGCCCATGGAGAGAC
TGCCTGCAGGCCCTGGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACACCAACCGCCTC
ATGCAGGTGTGGTGCGACCAGAGACACGACCCCGGGGGCTGGACCGTCATCCAGAGACGCCTGGATGGCTCTGTT
AACTTCTTCAGGAACCTGGGAGACGTACAAGCAAGGTTTGGGAACATTGACGGCGAATACTGGCTGGGCCTGGAG
AACATTTACTGGCTGACGAACCAAGGCAACTACAACTCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTC
TTTGAGAATACGCCAGTTTCCGCCTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGC
AATGCGGGTGACTCCTTTACATGGCACAACGGCAAGCAGTTCAACACCCTGGACAGAGATCATGATGTCTACACA
GGAAACTGTGCCCACTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCCACTCCAACCTCAACGGGGTCTGG
TACCGCGGGGGCCATTACCGGAGCCGCTACCAGGACGGAGTCTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA
CTCAAGAAAGTGGTGATGATGATCCGACCGAACCCCAACACCTTCCACTTAAGCCAGCTCCCCCTCCTGACCTCTC
GTGGCCATTGCCAGGAGCCCACCCTGGTCACGCTGGCCACAGCACAAAGAACAACCTCCTACCAGTTCATCCTGA
GGCTGGGAGGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAAGTGAATCGATACGGT
GTTTTCTGTCCCTCCTACTTTCTTTACACCAGACAGCCCCCTCATGTCTCCAGGACAGGACAGGACTACAGACAA
CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA

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FIGURE 268

MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQQ
RVTGAICVNSKEPEVLLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEVKLLRKE
SRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLEHKYQHLATL
AHNQSEIIAQLEEHQCRVPSARVPVQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNLKVLP
PPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQRHDPGG
WTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQGNKLLVTMEDWSGRKVF
AEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNAHYQKGGWYWN
ACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVMMIRPNPNTFH

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation sites:

amino acids 164-168, 192-196

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 124-128

Tyrosine kinase phosphorylation sites:

amino acids 177-184, 385-393, 385-394, 461-468

N-myristoylation sites:amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347, 465-471,
473-479**Amidation site:**

amino acids 373-377

Fibrinogen beta and gamma chains C-terminal domain signature:

amino acids 438-451

Fibrinogen beta and gamma chains C-terminal domain proteins:

amino acids 305-343, 365-402, 411-424, 428-458

Trehalase proteins:

amino acids 275-292

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FIGURE 269

GCCGAGCTGAGCGGATCCTCACATGACTGTGATCCGATTCTTTCCAGCGGCTTCTGCAACCAA
GCGGGTCTTACCCCCGGTCTCCGCGTCTCCAGTCTCGCACCTGGAACCCCAACGTCCCCGA
GAGTCCCCGAATCCCCGCTCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGGC
AGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTCAGGGCGGACCCGTGCAGTC
CAAGTCGCCCGCGCTTTGCGTCTTGGGACGAGATGAATGTCTGGCGCACGGACTCCTGCAGCT
CGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGACGTCAGCTGAGCGCGCTGGAGCGGGC
CCTGAGCGCGTGCGGGTCCGCCTGTGAGGGAACCGAGGGGTCCACCGACCTCCCGTTAGCCCC
TGAGAGCCGGGTGGACCCTGAGGTCTTTCACAGCCTGCAGACACAACCTCAAGGCTCAGAACAG
CAGGATCCAGCAACTCTTCCACAAGGTGGCCACGACGAGCGGCACCTGGAGAAGCAGCACCT
GCGAATTCAGCATCTGCAAAGCCAGTTTGGCCTCCTGGACCACAAGCACCTAGACCATGAGGT
GGCCAAGCCTGCCCCAAGAAAGAGGGCTGCCCCAGATGGCCCAGCCAGTTGACCCGGCTCACAA
TGTCAGCCGCCTGCACCGGCTGCCCAGGGATTGCCAGGAGCTGTTCCAGGTTGGGGAGAGGCA
GAGTGGACTATTTGAAATCCAGCCTCAGGGGTCTCCGCCATTTTTGGTGAACCTGCAAGATGAC
CTCAGATGGAGGCTGGACAGTAATTCAGAGGCGCCACGATGGCTCAGTGGACTTCAACCGGCC
CTGGGAAGCCTACAAGGCGGGGTTTGGGGATCCCCACGGCGAGTTCTGGCTGGGTCTGGAGAA
GGTGCATAGCATCACGGGGGACCGCAACAGCCGCCTGGCCGTGCAGCTGCGGGACTGGGATGG
CAACGCCGAGTTGCTGCAGTTCTCCGTGCACCTGGGTGGCGAGGACACGGCCTATAGCCTGCA
GCTCACTGCACCCGTGGCCGGCCAGCTGGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGT
ACCCTTCTCCACTTGGGACCAGGATCACGACCTCCGCAGGGACAAGAACTGCGCCAAGAGCCT
CTCTGGAGGCTGGTGGTTTGGCACCTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTC
CATCCCACAGCAGCGGCAGAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCGGCTA
CTACCCGCTGCAGGCCACCACCATGTTGATCCAGCCCATGGCAGCAGAGGCAGCCTCCTTAGCG
TCCTGGCTGGGCCTGGTCCCAGGCCCACGAAAGACGGTGACTCTTGGCTCTGCCCCAGGATGT
GGCCGTTCCTGCCTGGGCAGGGGCTCCAAGGAGGGGCCATCTGGAACTTGTGGACAGAGAA
GAAGACCACGACTGGAGAAGCCCCCTTTCTGAGTGCAGGGGGGCTGCATGCGTTGCCTCCTGA
GATCGAGGCTGCAGGATATGCTCAGACTCTAGAGGCGTGGACCAAGGGGCATGGAGCTTCACT
CCTTGCTGGCCAGGGAGTTGGGGACTCAGAGGGACCACTTGGGGCCAGCCAGACTGGCCTCAA
TGGCGGACTCAGTCACATTGACTGACGGGGACCAAGGGCTTGTGTGGGTGAGAGCGCCCTCAT
GGTGCTGGTGTGTTGTGTGTAGGTCCCCTGGGGACACAAGCAGGCGCCAATGGTATCTGGGC
GGAGCTCACAGAGTTCTTGAATAAAAGCAACCTCAGAACAC

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FIGURE 270

MTVIRFFPAASATKRVLPVLRVSSPRTWNPVPEPRIPAPRLPKRMSGAPTAGAALMLCAA
TAVLLSAQGGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAERTRSQLSALERRLSACGSA
CQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLFHKVAQQQRHLEKQHLRIQHLS
QFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSRLHRLPRDCQELFQVGERQSGLFELQ
PQGSPPFLVNCKMTSDGGWTVIQRRHDGSVDFNRPWEAYKAGFGDPHGEFWLGLEKVHSITGD
RNSRLAVQLRDWDGNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPPSGLSVPFSTWDQ
DHDLRDKNCAKSLSGGWWFGTCSHSNLNGQYFRSIPQQRQKLKKGIFWKTWRGRYYPLQATT
MLIQPMAAEAAS

Important features:**Signal peptide:**

Amino acids 1-13

Transmembrane domain:

Amino acids 53-70

N-glycosylation site:

Amino acids 224-228

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 46-50;118-122

N-myristoylation sites:

Amino acids 50-56;129-135;341-347;357-363

Fibrinogen beta and gamma chains C-terminal domain signature:

Amino acids 396-409

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FIGURE 271

CGGACGCGTGGGGGAAACCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGGG
AACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGCTG
CTGCTGCTGACCATGGCCTTGGCCGGAGGTTTCGGGGACCGCTTCGGCTGAAGCATTGACTCG
GTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACACCTAC
CCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTT
GTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTCGCT
GAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAATGCACCTACTCTTTCCTCTAACT
CTGGTGAGGTCATTCTGGAGTGACATGATGGAC TCCGCACAGAGCTTCATAACCTCTTCATGG
ACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCCAGAAATCCAG
TACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAAGCAAAATGTCC
TATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGAGAAAGTGATGGC
TTTTTAAGATGCCTCTCTCTTA ACTCTGGGTGGATTTTAACTACA ACTCTTGTCTCTCGGTG
ATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGCAGTATGTTCCTCT
GAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAGCTAAACAGATATCCA
GCTTCTTCTCTTGTGGTTGTTAGATCTAAACTGAAGATCATGAAGAAGCAGGGCCTCTACCT
ACAAAAGTGAATCTTGCTCATTCTGAAATTTTAAGCATTTTTCTTTTAAAGACAAGTGTAATA
GACATCTAAAATTCACCTCCTCATAGAGCTTTTAAAATGGTTTCATTGGATATAGGCCTTAAG
AAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

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FIGURE 272

MAAPKGS LWVRTQLGLPPLLLLTMALAGGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYPK
EEELYACQRCRLFSICQFVDDGIDLNRKLECESACTEAYSQSDEQYACHLGCQNQLPFAEL
RQEQLMSLMPKMHLLFPLTLVRSFWS DMMDSAQSFITSSWTFY LQADDGKIVIFQSKPEIQYA
PHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVLSVMV
LLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVR SKTEDHEEAGPLPTK
VNLAHSEI

Important features:**Signal peptide:**

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site:

amino acids 90-94

N-myristoylation sites:

amino acids 28-34, 29-35, 31-37, 86-92

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FIGURE 273

CCCACGCGTCCGAACCTCTCCAGCGATGGGGAGCCGCCCGCCTGCTGCCCAACCTCACTCTGTG
CTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACCGA
CCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCACGT
GCAGGTACCCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGCTCAT
AGTGGAGACGGACACGTTTGGCAGCCGGGTTTCGCATCAAAGGGGGCTGAGAGTGAGAAGTACAT
CTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCAGCGGGAAGAGCAAAGACTGCGTGTT
CACGGAGATCGTGCTGGAGAACAACCTATACGGCCTTCCAGAACGCCCGGCACGAGGGGCTGGTT
CATGGCCTTCACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAACCAGCGCGA
GGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCACGCCGAGAAGCA
GAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGGACCAAGCGCACACGGCGGCCCCA
GCCCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCCCTGGGCGCCTCCCCACCCCTTTCC
CTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCCGAGGGAGGACCC
TGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTGCCCCAGGGGCGGC
TGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACCTGAGTGTCACCCTGA
TCTCAGGCCACCAGCCTCTGCCGGCCTCCCAGCCGGGCTCCTGAAGCCCGCTGAAAGGTCAGC
GACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCCTCAAAATCTGCTTCTCGGATCT
CCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTAGGAAGGGACTTTTGTTT
GTTTGTTTGTTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAATAGAGGGTTGTCCACTCCTCA
CATTCACGACCCAGGCCTGCACCCCAACCCCAACTCCCAGCCCCGGAATAAAACCATTTTCC
TGC

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FIGURE 274

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRIS
ATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLGKPSGKSKDCVFTEIVLENN
YTAFQONARHEGWFMATRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEFVGS
APTRRTKRTRRPQPLT

Important features:**Signal peptide:**

Amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

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FIGURE 275

TATTTACCATATCAGATTCACATTCAGTCCTCAGCAAAATGAAGGGCTCCATTTTCACTCTGT
TTTTATTCTCTGTCCTATTTGCCATCTCAGAAGTGCGGAGCAAGGAGTCTGTGAGACTCTGTG
GGCTAGAATACATACGGACAGTCATCTATATCTGTGCTAGCTCCAGGTGGAGAAGGCATCTGG
AGGGGATCCCTCAAGCTCAGCAAGCTGAGACAGGAACTCCTTCCAGCTCCCACATAAACGTG
AGTTTTCTGAGGAAAATCCAGCGCAAAACCTTCCGAAGGTGGATGCCTCAGGGGAAGACCGTC
TTTGGGGTGGACAGATGCCCCACTGAAGAGCTTTGGAAGTCAAAGAAGCATTCACTGATGTCAA
GACAAGATTTACAACTTTGTGTTGCACTGATGGCTGTTCCATGACTGATTTGAGTGCTCTTT
GCTTAAGACAAGAGCAAATACCCAATGGGTGGCAGAGCTTTATCACATGTTTAATTACAGTGTT
TTACTGCCTGGTAGAACACTAATATTGTGTTATTAAAATGATGGCTTTTGGGTAGGCAAACT
TCTTTTCTAAAAGGTATAGCTGAGCGGTTGAAACCACAGTGATCTCTATTTTCTCCCTTTGCC
AAGGTTAATGAACTGTTCTTTTCAAATTCTACTAATGCTTTGAAATTTCAAATGCTGCGCAA
ATTGCAATAAAAATGCTATAAA

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FIGURE 276

MKGSIFTLFLFSVLFAISEVRSKESVRLCGLEYIRTVIYICASSRWRRLHLEGIPQAQQAETGN
SFQLPHKREFSEENPAQNLPKVDASGEDRLWGGQMPTEELWKSKKHSVMSRQDLQTLCTDGC
SMTDLSALC

Important features:

Signal sequence:

amino acids 1-18

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 107-111

N-myristoylation sites:

amino acids 3-9, 52-58, 96-102, 125-131

Insulin family signature:

amino acids 121-136

Insulin family proteins:

amino acids 28-46

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FIGURE 277

GCAGCTGGTTACTGCATTTCTCCATGTGGCAGACAGAGCAAAGCCACAACGCTTTCTCTGCTGGATTAAAGACGG
CCCACAGACCAGAACTTCCACTATACTACTTAAAATTACATAGGTGGCTTGTCAAATTCAATTGATTAGTATTGT
AAAAGGAAAAAGAAGTTCTTCTTACAGCTTGGATTCAACGGTCCAAAACAAAATGCAGCTGCCATTAAAGTCT
CAGATGAACAACTTCTACACTGATTTTTAAAATCAAGAATAAGGGCAGCAAGTTTCTGGATTCACTGAATCAAC
AGACACAAAAAGCTGGCAATATAGCAACTATGAAGAGAAAAAGCTACTAATAAAATTAACCCACGCATAGAAGAC
TTTTTTTTCTCTTCTAAAAACAATAAGTAAAGACTTAAATTTAAACACATCATTTTACAACCTCATTTCAAAT
GAAGACTTTTACCTGGACCCTAGGTGTGCTATTCTTCCCTACTAGTGGACACTGGACATTGCAGAGGTGGACAATT
CAAAATTAAAAAATAAACCCAGAGAAGATACCTCGTGCCACAGATGGTAAAGAGGAAGCAAAGAAATGTGCATA
CACATTCCTGGTACCTGAACAAAGAATAACAGGGCCAATCTGTGTCAACACCAAGGGGCAAGATGCAAGTACCAT
TAAAGACATGATCACCAGGATGGACCTTGAACCTGAAGGATGTGCTCTCCAGGCAGAAGCGGGAGATAGATGT
TCTGCAACTGGTGGTGGATGTAGATGGAAACATTGTGAATGAGGTAAAGCTGCTGAGAAAGGAAAGCCGTAACAT
GAACTCTCGTGTTACTCAACTCTATATGCAATTATTACATGAGATTATCCGTAAGAGGGATAATTCACCTGAACT
TTCCCAACTGGAAAACAAAATCCTCAATGTCAACACAGAAATGTTGAAGATGGCAACAAGATACAGGGAAGTACA
GGTGAAATACGCTTCTTGACTGATCTGTGTCATAAACCATCTGTGATGATCACTTGTGGAAGAAGTGTGCTT
GAGGATATTTTCCCGACAAGACACCCATGTGTCTCCCCACTTGTCCAGGTGGTGCCACAACATATTCCTAACAG
CCAACAGTATACTCCTGGTCTGCTGGGAGGTAACGAGATTCAAGAGGATCCAGGTTATCCCAGAGATTTAATGCC
ACCACCTGATCTGGCAACTTCTCCCACCAAAGCCCTTTCAAGATACCACCGGTAACCTTCATCAATGAAGGACC
ATTCAAAGACTGTCAGCAAGCAAAAGAAGCTGGGCATTCCGTCAGTGGGATTATATGATTAAACCTGAAAACAG
CAATGGACCAATGCAGTTATGGTGTGAAAACAGTTTGGACCCTGGGGGTTGGACTGTTATTTCAGAAAAGAACAGA
CGGCTCTGTCAACTTCTTCAGAAATTTGGGAAAATTATAAGAAAGGGTTTGGAAACATTGACGGAGAATACTGGCT
TGGACTGGAAAATATCTATATGCTTAGCAATCAAGATAATTACAAGTTATTGATTGAATTAGAAGACTGGAGTGA
TAAAAAAGTCTATGCAGAATACAGCAGCTTTCGTCTGGAACCTGAAAGTGAATTCATAGACTGCGCCTGGGAAC
TTACCAGGGAAATGCAGGGGATTCTATGATGTGGCATAATGGTAAACAATTCACCACACTGGACAGAGATAAAGA
TATGTATGCAGGAACTGCGCCCACTTTTATAAAGGAGGCTGGTGGTACAATGCCTGTGCACATTCTAACCTAAA
TGGAGTATGGTACAGAGGAGGCCATTACAGAAGCAAGCACCAGATGGAATTTTCTGGGCCGAATACAGAGGCGG
GTCATACTCCTTAAGAGCAGTTCAGATGATGATCAAGCCTATTGACTGAAGAGAGACACTCGCCAATTTAAATGA
CACAGAACTTTGTACTTTTTCAGCTCTTAAAAATGTAAATGTTACATGTATATTACTTGGCACAATTTATTTCTAC
ACAGAAAGTTTTTAAATGAATTTTACCGTAACCTATAAAGGGAACCTATAAATGTAGTTTCATCTGTCTGCTCAAT
TACTGCAGAAAATTATGTGTATCCACAACCTAGTTATTTTAAAAATATGTTGACTAAATACAAAGTTTGTTTTC
TAAATGTAAATATTTGCCACAATGTAAAGCAAATCTTAGCTATATTTTAAATCATAAATAACATGTTCAAGATA
CTTAACAATTTATTTTAAATCTAAGATTGCTCTAACGTCTAGTGAAAAAATATTTTTTAAATTTTCAAGCAAATA
ATGCATTTTATTTTATAAATAACAGACAGAAAATTAGGGAGAAAATCTAGTTTGGCAATAGAAAATGTTCTT
CCATTGAATAAAAGTTATTTCAAATTTGAATTTGTGCCTTTCACACGTAATGATTAAATCTGAATTTCTAATAATA
TATCCTATGCTGATTTTCCCAAACATGACCCATAGTATTAAATACATATCATTTTTTAAAAATAAAAAAAACCC
AAAAATAATGCATGCATAATTTAAATGGTCAATTTATAAAGACAAATCTATGAATGAATTTTTTCACTGTTATCTT
CATATGATATGCTGAACACCAAATCTCCAGAAATGCATTTTATGTAGTTCTAAATCAGCAAAATATTGGTATT
ACAAAAATGCAGAAATATTTAGTGTGCTACAGATCTGAATTATAGTTCTAATTTATTATTACTTTTTTTCTAATTT
ACTGATCTTACTACTACAAAGAAAAAAAACCCAAACCATCTGCAATTCAAATCAGAAAGTTTGGACAGCTTTAC
AAGTATTAGTGCATGCTCAGAACAGGTGGGACTAAAACAACTCAAGGAAGTGTGGCTGTTTTCCCGATACTGA
GAATTCAACAGCTCCAGAGCAGAAGCCACAGGGGCATAGCTTAGTCCAACTGCTAATTTTCACTTTTACAGTGTAT
GTAACGCTTAGTCTCACAGTGTCTTTAACTCATCTTTGCAATCAACAACCTTTACTAGTGACTTTCTGGAACAATT
TCCTTTTCAGGAATACATATTTACTGCTTAGAGGTGACCTTGCTTAAATATATTTGTGAAGTTAAAAATTTTAAAGA
TAGTCTCATGAACTTTTGTCTAAGCAAAAAGAAAACCTCGAATTGAAATGTGTGAGGCAAACTATGCATGGGAAT
AGCTTAATGTGAAGATAATCATTTGGACAACCTCAAATCCATCAACATGACCAATGTTTTTTCATCTGCCACATCTC
AAAAATAAACTTCTGGTGAAACAAATTAAACAAAATATCCAAACCTCAAAAAA

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FIGURE 278

MKTFTWTLGVLFLLVDTGHCRRGGQFKIKKINQRRYPRATDGKEEAKKCAYTFLVPEQRITGP
ICVNTKGQDASTIKDMITRMDLENLKDVLRSQKREIDVLQLVVDVDGNIVNEVKLLRKESRNM
NSRVTQLYMQLLHEIIRKRDNSLELSQLENKILNVTTEMLKMATRYRELEVKYASLTDLVNNQ
SVMITLLEEQCLRIFSRQDTHVSPPLVQVVPQHIPNSQQYTPGLLGGNEIQRDPGYPRDLMPP
PDLATSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIYMIKPENSNGPMQLWCENSLDP
GGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYWLGLENIYMLSNQDNYKLLIELEDWSDKK
VYAEYSSFRLEPESEFYRLRLGTYQGNAGDSMMWHNGKQFTTLDRDKDMYAGNCAHFHKGWW
YNACAHSNLNGVWYRGGHYRSKHQDGI FWA EYRGGSYS LRAVQMMIKPID

Important features:**Signal sequence:**

Amino acids 1-23

N-glycosylation sites:

Amino acids 160-164;188-192

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 120-124

Tyrosine kinase phosphorylation sites:

Amino acids 173-180;387-396

N-myristoylation sites:Amino acids 70-76;110-116;232-238,343-349;400-406;467-473;
475-487**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 440-453

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FIGURE 279

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCTGCCAGTCTCGCCCGCGATCCCGGC
CCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGCCG
CCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGCGGAGAAGCC
CGGGCAAACGCAGGCTAAGGAGACCAAAGCGGGCGAAGTCGCGAGACAGCGGACAAGCAGCGGA
GGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGGCGTCG
TGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCGAGCGCG
AGAAATCCAACGCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGCGACAAAA
ACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGGCGCAGAAGAAGAC
CAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACCACTTGCAGC
TGCAGGCGGATGGAACCATTTGATGGCACCAAGATGAGGACAGCACTTACACTCTGTTTAACC
TCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCTGTACTTGGCAA
TGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTCACACCTGAGTGCAAATTCAAAGAAT
CAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAGCAGCAGTCAGGCC
GAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAACCATGTGAAGAAGA
ACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGTACAAGGAGCCATCAC
TGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACCAAGAGCAGAAGTGTCT
CTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAACGTAGCCAGTGAGGGCAA
AAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAATTCTTCTAGCAGTCCTTCA
CCCAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGGCAGAGTTCACTATTCTATC
TGCCATTAGACCTTCTTATCATCCATACTAAAGC

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FIGURE 280

MAAAIASSLI RQKRQAREREKSNACKCVSSPSKGKTS CDKNKLN VF SRVKLFGSKKRRRRRPE
PQLKGIVTKLYSRQGYHLQLQADGTIDGTKDEDSTYTLFNLI PVGLRVVAIQGVQTKLYLAMN
SEGILYTSSELTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVKKNK
PAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLN GGKSM SHNEST

Important Features:**N-glycosylation site:**

Amino acids 242-246

Glycosaminoglycan attachment sites:

Amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site:

Amino acids 93-100

N-myristoylation sites:

Amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop):

Amino acids 231-239

HBGF/FGF family proteins:

Amino acids 78-94, 102-153

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FIGURE 281

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGGA
CTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGGCA
ACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCTCCA
TTTAGAGTGTAGCAAAGGAAAAACACCAAGGTTGGGTTCCCTTCCTGACATTGGCAGTGCCCC
AGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCACACCCTGTAGATTACAAGAG
TGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAAACCACG
TCTTGGAATTTAGTGGGTCTTGCTTTGGGATAGGTGAAGTGAGGACAGACACTGGAGAGGA
GGGAAAGGGGACGTTTTCAATAGGAGGCCAAACTCGAGGGTGGGATCCACTGAGGAGTACATA
GGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACTGGCTGCTGTGGAGGGG
GGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAGCGAGTCGGGG
CCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAGCGCGCTCCGGG
CGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGGCGGCGCTGGCCAGTAGCCTGAT
CCGGCAGAAGCGGGAGGTCCGCGAGCCCCGGGGGCAGCCGGCCGGTGTGCGGCGAGCGGCGCGT
GTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTGCTGTCCAAGGTGCG
ACTGTGCGGGGGGCGGCCCCGCGCGGCCGACCGCGGCCCGGAGCCTCAGCTCAAAGGCATCGT
CACCAAAGTGTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCGACGGAAGCATCCAGGG
CACCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCTGTGGGCCTCCGTGTGGT
CACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGCTGAGGGACTGCTCTACAG
TTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCTTTGAGAATTACTACGTCCT
GTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCCTGGTACCTCGGCCTGGACAA
GGAGGGCCAGGTCATGAAGGGAAACCGAGTTAAGAAGACCAAGGCAGCTGCCCCACTTTCTGCC
CAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCCACAGTGTCCCCGAGGCCTCCCC
TTCCAGTCCCCCTGCCCCCTGAAATGTAGTCCCTGGACTGGAGGTTCCCTGCACTCCCAGTGA
GCCAGCCACCACCACAACCTGT

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FIGURE 282

MAALASSLIRQKREVPGGSRPVSAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDRG
PEPQLKGIVTKLFCRQGFYQLQANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHYMA
MNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNRVKK
TKAAAHFLPKLLEVAMYQEPSLHSVPEASPSSPPAP

Important features:**Tyrosine kinase phosphorylation site:**

Amino acids 199-207

N-myristoylation sites:

Amino acids 54-60; 89-95; 131-137

HBGF/FGF family signature:

Amino acids 131-155

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FIGURE 283

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTGG
GACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACGGC
AACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGGCGC
CAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTTGCAA
ATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCTTCAAC
CTCATAACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTATATAGCC
ATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTTTAAAGAA
TCTGTTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGGAATCTGGT
AGAGCCTGGTTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGAGTAAAGAAA
ACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCGAGAACCATCT
TTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAAGCACAAGTGCG
TCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACA**TAG**

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FIGURE 284

MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLRR
QDPQLKGIVTRLYCRQGYYLQMHPDGALDGTKDDSTNSTLFNLIPVGLRVVAIQGVKTGLYIA
MNGEGYLYPSELFTECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNRVKK
TKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSITT

Important features:**N-glycosylation sites:**

Amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site:

Amino acids 199-207

N-myristoylation sites:

Amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins:

Amino acids 104-155, 171-198

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FIGURE 285

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTTCAGGTCCAGGTTTTGCTTTGA
TCCTTTTCAAAAACCTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAACTACCCT
GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAAGAGAC
TCGGGAGTCGCTGCTTCCAAAGTGCCCCGCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGC
TTCTCCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTCC
AGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG
GAAGTATTCACAGCCCCAAGGTTTCCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG
AGGAAAATGTATGGATACAACCTTACGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT
ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAACCTATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAG
GAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCAGGGT
TCTGCATCCACTACAACATTGTCATGCCACAATTCACAGAAGCTGTGAGTCCTTCAGTGCTACCCCCCTTCAGCTT
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGGGAAGACCTTATTCGATATCTTGAACCAG
AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAAGCTTGGCAACTTCTTGGCAAGGCTTTTGTTTTGGAA
GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCT
CAGTGTCCATAAGGGAAGAATAAAGAGAACCGATAACATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTG
GTGGGAAGTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC
ACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTACCGACGTGGCCCTGGAGC
ACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCA
GAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCT
TCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA
ACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAGAAAATTAATGTTGTAT
TAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCAGTACTGAGTGGGTTCTGTATTTTCAGTTCTTTC
GATACGGCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCGTTGCCTTGCTTAAC
TCTAAAGCTCCATGTCCTGGGCCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTGCTCATATTCACAT
ATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAAGTATGTTGCTATGAATTAACCTGT
GTCATGCTGATAGGACAGACTGGATTTTTTCATATTTCTTATTAATTTCTGCCATTTAGAAGAAGAGAACTACA
TTCATGGTTTGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTG
TTTCATTGTGTACATTTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCT
ATTTTTACCAAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGGTAAATTTTTCT
AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA
TTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAA
GACTTTTTGAAAAATAATTAAATTATCATATCTTCCATTCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGA
AAGTAGACATTTCAGATCCAGCCATTACTAACCTATTCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT
AAAGCACCTTGAAAAAGACTTGGCAGCTTCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCCTATTTA
TTGTGATGTTGTGGTTTTTATTATCTTAACTCTGTTCCATACACTTGATATAAATACATGGATATTTTTATGTACA
GAAGTATGTCTCTTAACCAGTTCACCTATTGTACTCTGGCAATTTAAAAGAAAATCAGTAAAATATTTTGCTTGT
AAAATGCTTAATATNGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAATAAAAAGA
ATGTGGCTATTTTGGGGAGAAAATTAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

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FIGURE 286

MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRF
PHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGS
GTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLLNNA
ITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRKSRVVDLNLLEEVRLYSCTP
RNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKT
GVRGLHKSITDVALEHHEECDVCVRGSTGG

Important features:**signal sequence:**

Amino acids 1-14

N-glycosylation sites:

Amino acids 25-29;55-59;254-258

N-myristoylation sites:

Amino acids 15-21;117-123;127-133;281-287;282-288;319-325

Amidation site:

Amino acids 229-233

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FIGURE 287

CAGCGCTGACTGCGCCGCGGAGAAAGCCAGTGGGAACCCAGACCCATAGGAGACCCGCGTCCC
CGCTCGGCCTGGCCAGGCCCCGCGCT**ATG**GAGTTCCTCTGGGCCCCCTCTCTTGGGTCTGTGCT
GCAGTCTGGCCGCTGCTGATCGCCACACCGTCTTCTGGAACAGTTCAAATCCCAAGTTCCGGA
ATGAGGACTACACCATAACATGTGCAGCTGAATGACTACGTGGACATCATCTGTCCGCACTATG
AAGATCACTCTGTGGCAGACGCTGCCATGGAGCAGTACATACTGTACCTGGTGGAGCATGAGG
AGTACCAGCTGTGCCAGCCCCAGTCCAAGGACCAAGTCCGCTGGCAGTGCAACCGGCCCAGTG
CCAAGCATGGCCCCGAGAAGCTGTCTGAGAAGTTCCAGCGCTTCACACCTTTCACCCTGGGCA
AGGAGTTCAAAGAAGGACACAGCTACTACTACATCTCCAAACCCATCCACCAGCATGAAGACC
GCTGCTTGAGGTTGAAGGTGACTGTCAGTGGCAAATCACTCACAGTCCTCAGGCCCCATGACA
ATCCACAGGAGAAGAGACTTGCAGCAGATGACCCAGAGGTGCGGGTTCTACATAGCATCGGTC
ACAGTGCTGCCCCACGCCTCTTCCCACTTGCCTGGACTGTGCTGCTCCTTCCACTTCTGCTGC
TGCAAACCCCG**TGA**AGGTGTGTGCCACACCTGGCCTTAAAGAGGGACAGGCTGAAGAGAGGGA
CAGGCACTCCAAACCTGTCTTGCGGCCACTTTCAGAGCCCCCAGCCCTGGGAACCACTCCCAC
CACAGGCATAAGCTATCACCTAGCAGCCTCAAACGGGTCAATATTAAGGTTTTCAACCGGAA
GGAGGCCAACCAGCCCGACAGTGCCATCCCCACCTTCACCTCGGAGGGATGGAGAAAGAAGTG
GAGACAGTCCTTTCCCAACCATTCCTGCCTTTAAGCCAAAGAAACAAGCTGTGCAGGCATGGTC
CCTTAAGGCACAGTGGGAGCTGAGCTGGAAGGGGCCACGTGGATGGGCAAAGCTTGTCAAAGA
TGCCCCCTTCAGGAGAGAGCCAGGATGCCCAGATGAACTGACTGAAGGAAAAGCAAGAAACAG
TTTCTTGCTTGGAAGCCAGGTACAGGAGAGGCAGCATGCTTGGGCTGACCCAGCATCTCCCAG
CAAGACCTCATCTGTGGAGCTGCCACAGAGAAGTTTGTAGCCAGGTACTGCATTCTCTCCCAT
CCTGGGGCAGCACTCCCCAGAGCTGTGCCAGCAGGGGGGCTGTGCCAACCTGTTCTTAGAGTG
TAGCTGTAAGGGCAGTGCCCATGTGTACATTCTGCCTAGAGTGTAGCCTAAAGGGCAGGGCCC
ACGTGTATAGTATCTGTATATAAGTTGCTGTGTGTCTGTCCTGATTTCTACAACCTGGAGTTTT
TTTATACAATGTTCTTTGTCTCAAATAAAGCAATGTGTTTTTTCGG

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FIGURE 288

MEFLWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM
EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEGHSYY
YISKPIHQHEDRCLRLKVTVSGKITHSPQAHNPNQEKRLAADDPEVRVLHSIGHSAAPRLFPL
AWTVLLLLPLLLLQTP

Important features:**Signal sequence:**

Amino acids 1-17

N-glycosylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 118-127

N-myristoylation site:

Amino acids 10-16

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FIGURE 289

CGGACGCGTGGGCGGACGCGTGGGCGGCCCCACGGCGCCCGCGGGCTGGGGCGGTGCTTCTTC
CTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGGCCCCATGGCCCCCGAAGGGC
CTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGGCTC
CAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTGCCGG
GGA CTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAAC TTTGGAGGTGGA
AACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTGGTAGAG
GTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCTGAGTGAG
GAGCTGGTGGAGAGCTGGTGGTTTCAACAAGCAGCAGGAGGCCCCGGACCTCTTCCAGTGGCTG
TGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGGCCCTCCTGCCTTCCCTGT
CCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGGGACACGAGGG
GGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCCAGTGTGGCCTT
GGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGTTTTGGCCCCCTGT
GCCCGATGCTCAGGACCTGAGGAATCAAAC TGTTCGCAATGCAAGAAGGGCTGGGCCCTGCAT
CACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACTGTGGAGCTGACCAA
TTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAGGCCTGCCTAGGCTGC
ATGGGGGCAGGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCAGCAGGTGGGCTCCAAG
TGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGAACAAGCAGTGTGAAAAC
ACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAGATGGAAGGCATCTGTGTG
AAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGACAGAAGACGAGTTGGTGGTG
CTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCACGCTGGCTGCTAAGGGCGAC
TTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATGACTGGCTACTGGTTGTCAGAG
CGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATTAATCGCGGCCACCACCTGTAGGA
CCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGCTGCCCTCCTGCTGGACACTCAGGACAGC
TTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTGCCTTACAGAGCAGCCCAGGTACCC
AGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGCCCTGAAGGTGGATACCATGAGCTCT
TCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGAATTTCAAAAGTTTTTCCTTAATGGTG
GCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTGGTCCCTCACAGGGGTGGGGCCATCACAG
CTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGTTCTGTGTTACCCACATCCCCACACCCCA
TTGCCACTTATTTATTCATCTCAGGAAATAAAGAAAGGTCTTGGAAGTTAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 290

MAPWPPKGLVPAVLWGLSLFLNLPGPPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLERT
IRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQQE
APDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDQCAGYGG
EACGQCGLGYFEAERNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDECGTE
GANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECETEVCP
GENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVLVQLQMFFGIICAL
ATLAAKGDVFTAFIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Important features:**Signal sequence:**

Amino acids 1-29

Transmembrane domain:

Amino acids 342-392

N-glycosylation sites:

Amino acids 79-83;205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 290-294

Aspartic acid and asparagine hydroxylation site:

Amino acids 321-333

EGF-like domain cysteine pattern signature:

Amino acids 181-193

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FIGURE 291

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGACCCAC
GCGTCCGAACACAGGTCCTTGTTGCTGCAGAGAAGCAGTTGTTTTGCTGGAAGGAGGGAGTGCGCGGGCTGCCCC
GGGCTCCTCCCTGCCGCTCCTCTCAGTGGATGGTTCCAGGCACCCTGTCTGGGGCAGGGAGGGACAGGCCTGC
ACATCGAAGGTGGGGTGGGACCAGGCTGCCCCCTGCCCCAGCATCCAAGTCCTCCCTTGGGCGCCCGTGGCCCTG
CAGACTCTCAGGGCTAAGGTCCTCTGTTGCTTTTTGGTTCCACCTTAGAAGAGGCTCCGCTTGACTAAGAGTAGC
TTGAAGGAGGCACCAATGCAGGAGCTGCATCTGCTCTGGTGGGCGCTTCTCCTGGGCTGGCTCAGGCCTGCCCTG
AGCCCTGCGACTGTGGGAAAAGTATGGCTTCCAGATCGCCGACTGTGCCTACCGCGACCTAGAATCCGTGCCGC
CTGGCTTCCCGGCCAATGTGACTACACTGAGCCTGTGAGCCAACCGGCTGCCAGGCTTGCCGGAGGGTGCCCTCA
GGGAGGTGCCCCCTGCTGCAGTCGCTGTGGCTGGCACACAATGAGATCCGCACGGTGGCCGCCGGAGCCCTGGCCT
CTCTGAGCCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTCTGACTTTGCCTGGAGCGACCTGCACAACC
TCAGTGCCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCCGCGACGCCTTCCGCAGCCTCC
GTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGACACATTGGCCGAGGGACCTTCACCCCGCTCACC
CGCTGTCCCACCTGCAGATCAACGAGAACCCTTCGACTGCACCTGCGGCATCGTGTGGCTCAAGACATGGGCCC
TGACCACGGCCGTGTCCATCCCGGAGCAGGACAACATCGCCTGCACCTCACCCTCATGTGCTCAAGGGTACACCGC
TGAGCCGCTGCCGCCACTGCCATGCTCGGCGCCCTCAGTGCAGCTCAGCTACCAACCCAGCCAGGATGGTGGCG
AGCTGCGGCTGGTTTTGTGCTGGCACTGCACTGTGATGTGGACGGGAGCCGGCCCTCAGCTTCACTGGCACA
TCCAGATACCCAGTGGCATTGTGGAGATCACCAGCCCCAACGTGGGCACTGATGGGCGTGCCCTGCCTGGCACCC
CTGTGGCCAGCTCCCAGCCGCGCTTCCAGGCCTTTGCCAATGGCAGCCTGCTTATCCCCGACTTTGGCAAGCTGG
AGGAAGGCACCTACAGCTGCCTGGCCACCAATGAGCTGGGAGTGCTGAGAGCTCAGTGGACGTGGCACTGGCCA
CGCCCGGTGAGGGTGGTGAGGACACACTGGGGCGCAGGTTCCATGGCAAAGCGGTTGAGGGAAGGGCTGCTATA
CGGTTGACAACGAGGTGCAGCCATCAGGGCCGGAGGACAATGTGGTCATCATCTACCTCAGCCGTGCTGGGAACC
CTGAGGCTGCAGTCGCAGAAGGGTCCCTGGGCGAGCTGCCCCAGGCCTGCTCCTGCTGGGCGAAAGCCTCCTCC
TCTTCTTCTTCTCCTCAGCTCCTTCTAGCCCCACCCAGGGCTTCCCTAACTCCTCCCCCTTGCCCTACCAATGCCCC
TTTAAGTGCTGCAGGGGTCTGGGGTTGGCAACTCCTGAGGCCTGCATGGGTGACTTCACATTTTCTACCTCTCC
TTCTAATCTCTTCTAGAGCACCTGCTATCCCCAATTCTAGACCTGCTCCAACTAGTGAAGTAGGATAGAATTTG
ATCCCCCTAACTCACTGTCTGCGGTGCTCATTGCTGCTAACAGCATTGCCTGTGCTCTCCTCTCAGGGGAGCATG
CTAACGGGGCGACGTCTAATCCAATGGGAGAAGCCTCAGTGGTGGAATTCCAGGCACTGTGACTGTCAAGCTG
GCAAGGGCCAGGATTGGGGGAATGGAGCTGGGGCTTAGCTGGGAGGTGGTCTGAAGCAGACAGGGAATGGGAGAG
GAGGATGGGAAGTAGACAGTGGCTGGTATGGCTCTGAGGCTCCCTGGGGCCTGCTCAAGCTCCTCCTGCTCCTTG
CTGTTTTCTGATGATTTGGGGGCTTGGGAGTCCCTTTGTCCTCATCTGAGACTGAAATGTGGGGATCCAGGATGG
CCTTCCTTCTCTTACCCTTCTCCTCAGCCTGCAACCTCTATCCTGGAACCTGTCTCCTCCTTTCTCCCCAACT
ATGCATCTGTTGTCTGCTCCTCTGCAAAGGCCAGCCAGCTTGGGAGCAGCAGAGAAATAAACAGCATTCTGATG
CCAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCT

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FIGURE 292

MQELHLLWWALLLGLAQACPEPCDCGKEYGFQIADCAYRDLESVPPGFANVTTLSSLNRLP
GLPEGAFREVPLLQSLWLAHNEIRTVAAGALASLSHLKSLDLSHNLISDFAWSDLHNLSALQL
LKMDSNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINENPFDCTCGIV
WLKTWALTAVSIPEQDNIACTSPHVLKGTPLSRLPPLPCSAPSVQLSYQPSQDGAELRPGFV
LALHCDVDGQPAPQLHWHIQIPSGIVEITSPNVGTDGRALPGTPVASSQPRFQAFANGSLLIP
DFGKLEEGTYISCLATNELGSAESSVDVALATPGEGGEDTLGRRFHGKAVEGKGCYTVDNEVQP
SGPEDNVVIIYLSRAGNPEAAVAEGVPGQLPPGLLLLQSLLLFFFLTSE

Important features:**Signal peptide:**

amino acids 1-18

Transmembrane domain:

amino acids 403-418

N-glycosylation sites:

Amino acids 51-55, 120-124, 309-313

Tyrosine kinase phosphorylation site:

amino acids 319-326

N-myristoylation sites:amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329, 334-340,
350-356, 394-400**Amidation site:**

amino acids 355-359

Leucine Rich Repeat:

amino acids 51-74, 75-98, 99-122, 123-146, 147-170

Leucine rich repeat C-terminal domain:

amino acids 180-230

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FIGURE 293

ACTTGGAGCAAGCGGCGGGCGGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCTCGCCTCCCACGAGCG
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCCCTGCC
TCGCTTCCCAGGCGCCGGCGGCTGCAGCCTTGCCCCCTCTTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCT
GCTTCTGCTGATCCTCGGACAGATCGTTCCTCCTCCCTGCCGAGGCCAGGGAGCGGTACGTGGGAGGTCCATCT
CTAGGGGCAGACAGCTCGGACCCACCCGAGACGGCCCTTCTGGAGAGTTCCCTGTGAGAACAAGCGGGCAGACC
TGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTTCATCGTGGACA
TCTTGCAATTCTTGGACATTGGTCCTGATGTACCCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAATG
AGTTCCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGCTGTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGGGCGGCCCTGA
GGGAGAATGTGCCACGGGTCAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA
AGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCCAATTTAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCCCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAAGATCCAGGATCTGT
GTGCCATGGAGGACCACAACCTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAACACGGATGTGAAC
ATGAGTGTGTAAATGCTGATGGCTCCTACCTTTGCCAGTGCCATGAAGGATTGCTCTTAACCCAGATGAAAAA
CGTGCACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCGTCAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAACCTGCAGCCGAGTGGACCACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCTTCGTCTGCCAGTGCTCAGAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTGAGTGACCATGGTTGTGAATACTCCT
TGTCACCATGGACAGATCCTTTGCCCTGTCAGTGTCTGAGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG
CAAAATTGGACTCTTGTGCTCTGGGGGACACGGTTCCTGAGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG
GCCAGTGCTTTGAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTATAG
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATAACGTGCGAGTGCTTGGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAATCAACCCACCATGGCTGCCAACACATTTGTGTGA
ATAATGGGAATTCCTACATCTGCAATGCTCAGAGGGATTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAAT
GCACTGAAGCCCAATTGACCTGGTCTTTGTGATCGATGATCCAAGAGTCTTGGAGAAGAGAATTTTGAGGTGCTG
TGAAGCAGTTTGTCACTGGAATTATAGATTCTTTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAAAGCCGTGGCCC
ACATGAAATACATGGGAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTACCCAAG
GAGAAGGGGCCAGGCCCCCTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTTACCGACGGACGGGCTCAGGATG
ACGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG
AGGAGGAACATACAAGAGATTGCCTCTGAGCCCAACAAAGCATCTCTTCTATGCCGAAGACTTCAGCACAAATGG
ATGAGATAAGTGA AAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAAC TGCCAAAACGGTCCAACAGCCAACAGAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAATTTTGCACTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTT
CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCAAACGAAGAAGTAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC
TGGAAAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT
GAACGCAGTGCAGAGCCCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAAACAATCAGTACTGA
GAAACCTGGTTTGCCACAGAACAAGACAAGAAGTATACACTAACTTGTATAAATTTATCTAGGAAAAAAATCCT
TCAGAATTCTAAGATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACAC
AACTTGCTTCTGCCTCATCCTGCCTTAGTGTGCAATCTCATTTGACTATACGATAAAGTTTGCACAGTCTTACTT
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTGTACTGGACTTTACCTTGATATATGTATATGGATGTATG
CATAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATTAAATTCACCACTTCAG

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FIGURE 294

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFIID
SSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAVKR
MRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARDTGI
LIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHNCAHF
CINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYALAEDG
KRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGEHECVN
MEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLKTC
SRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRS DGKTC AKLDSCALGDHGCEHSCVSSD
SFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLAEDGKRCRRK
DVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVIDGSKSLGEENF
EVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVAHMKYMGKGSMT
GLALKHMFERSFTQEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKA
IEEELQEIASPTNKHLYAEDFSTMDEISEKLKKGICEALEDSDGRQDSPAGELPKTVQOPT
ESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPLEEKHDQCKCENLIM
FQNLANEEVRKLTQRLEEMTQORMEALENRLRYR

Important features:**Signal sequence:**

Amino acids 1-23

N-glycosylation site:

Amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 115-119; 606-610; 892-896

N-myristoylation sites:Amino acids 133-139; 258-264; 299-305; 340-346; 453-459; 494-500;
639-645; 690-694;
752-758; 792-798**Amidation sites:**

Amino acids 314-318; 560-564; 601-605

Aspartic acid and asparagine hydroxylation sites:Amino acids 253-265; 294-306; 335-347; 376-388; 417-429;
458-470; 540-552; 581-593

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FIGURE 295

GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACCCGC
CATGCGCCTGCCGCGCCGGGCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCCGCCCCG
GCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGACAAGTTTAA
CCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGCTTGGGAGGAAAA
GACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCTGGAGGGGCTGTGCGA
GAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGAGCACCTGGAGGCCTGGTG
GCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTTTGTGTGAAGACACTGAAAGT
GTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGATCCCAGAGGCC
CTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGGTCTGCCGGTG
CCACATGGGGTACCAGGGCCCCGCTGTGCACTGACTGCATGGACGGCTACTTCAGCTCGCTCCG
GAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCCTGCAAGACGTGCTCGGGCCTGAC
CAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGT
GGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGG
CTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAAA
CTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTG
CTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTA
CGTCTGTGTGTCTCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGC
TGAAGCCACAGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTG**TAA**TGTGCCGG
ACTTACCCTTTAAATTATTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCT
CCTGCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTGTCCC
TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTTTGT
AATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

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FIGURE 296

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEEK
TLSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLLKV
CCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLR
NETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPPCSAAQFCKNANG
SYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKTCVRKNENCYNTPGSY
VCVCPDGFEEETEDACVPPAAEAEATEGESPTQLPSREDL

Important features:**Signal peptide:**

Amino acids 1-24

N-glycosylation sites:

Amino acids 190-194;251-255

Glycosaminoglycan attachment sites:

Amino acids 149-153;155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 303-310

N-myristoylation sites:Amino acids 44-50;54-60;55-61;81-87;150-156;158-164;164-170;
252-258;313-319**Aspartic acid and asparagine hydroxylation site:**

Amino acids 308-320

EGF-like domain cysteine pattern signature:

Amino acids 166-178

Leucine zipper pattern:

Amino acids 94-116

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FIGURE 297

GACATCGGAGGTGGGCTAGCACTGAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAGAAAGAGAAAGAAGAGGAAG
ATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCTGGCATCATGCTGCTATTCTGCAAATACTGA
AGAAGCATGGGATTTAAATATTTTACTTCTAAATAAATGAATTACTCAATCTCCTATGACCATCTATACATACTC
CACCTTCAAAAAGTACATCAATATTATATCATTAAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTT
TTGGACAATGCAATTGTGGCACTGGCACTTATTTTCAGTGAAGAAAACTTTGTGGTTCTATGGCATTTCATCATTT
GACAAATGCAAGCATCTTCCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTGTGGAATCCTTAAGGGC
CCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACTCCGAATTCATGTGCTACTTGGCCTAGCTA
TCACTACACTAGTACAAGCTGTAGATAAAAAAGTGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGT
TTACACCCAGATCCATTTATATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCA
GATTGCCAGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAGACTTTC
CAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAATATTAATGTAAAAAAGATGC
CTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAACTTACTGAACTGCCTGAAAAATGTCTGTCCGAAGTGAAGCA
ACTTACAAGAACTCTATATTAATCACAACCTTGCTTTCTACAATTTACCTGGAGCCTTTATTGGCCTACATAATC
TTCTTCGACTTCATCTCAATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAG
AGATTCTGATGATTGGGGAAAATCCAATTATCAGAATCAAAGACATGAACTTTAAGCCTCTTATCAATCTTCGCA
GCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTTGGACTGGAAAACCTTAGAAAGCA
TCTCTTTTTACGATAACAGGCTTATTAAGTACCCCATGTTGCTCTTCAAAAAGTTGTAAATCTCAAATTTTTGG
ATCTAAATAAAAAATCCTATTAATAGAATACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGA
TAAATAATATGCCTGAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAG
CTACTAACAACCTAGATTGTCTTACATTACCCCAATGCATTTTTTCAGACTCCCCAAGCTGGAATCACTCATGC
TGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTGCCAAACCTCAAGGAAATCAGCATA
ACAGTAACCCCATCAGGTGTGACTGTGTCTATCCGTTGGATGAACATGAACAAAACCAACATTGATTTCATGGAGC
CAGATTCACTGTTTTGCGTGGACCCACCTGAATTCGAAGGTGAGAATGTTGCGCAAGTGCATTTACAGGGACATGA
TGGAAATTTGTCTCCCTCTTATAGCTCCTGAGAGCTTTCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGTTT
CCTTTCACTGTAGAGCTACTGCAGAACCACAGCCTGAAATCTACTGGATAACACCTTCTGGTCAAAAACCTCTTGC
CTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTAGATATAAATGGCGTAACCTCCCAAGAAG
GGGTTTTATATACTTGTATAGCAACTAACCTAGTTGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGAT
CTTTTCCACAAGATAACAATGGCTCTTTGAATATTAAATAAGAGATATTCAGGCCAATTCAGTTTTGGTGTCTT
GGAAAGCAAGTTCTAAAATTCTCAAATCTAGTGTTAAATGGACAGCCTTTGTCAAGACTGAAAATTCTCATGCTG
CGCAAAGTGCTCGAATAACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATCCATCAACTGAGTATAAAA
TTTGTATTGATATTCCCACCATCTATCAGAAAAACAGAAAAAATGTGTAAATGTCACCACCAAGGTTTGACC
CTGATCAAAAAGAGTATGAAAAGAATAATACCACAACACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTG
GTGTGATATGTCTTATCAGCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACT
TACAGAAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAAAGAAAAA
GTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCCTAAAAACCACCAAGGAAACCTA
CTCCAAAATGAAC

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FIGURE 298

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLTF
PARLPANTQILLQLQTNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLEEN
KLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRLQMINSKWFDALPN
LEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVP
HVALQKVVNLFKFLDLNKNPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLPLDRKIE
ATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISIHNSPIRCDCVIRW
MNMNKTNIRFMEPDSLFCVDPPEFQGQNVVRQVHFRDMMEICLPLIAPESFPSNLNVEAGSYVS
FHCRTAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTCIATNLVGA
DLKSVMIKVDGSEFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFAVKTENSHAAQ
SARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKEYEKNNTTTLM
ACLGGLLGIIGVICLISCLSPENNCDDGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKSTS
LKVKATVIGLPTNMS

Important features:**Signal sequence:**

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708**Cell attachment sequence.**

amino acids 277-280

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FIGURE 299

GCTGTGGGAACCTCTCCACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGAGTT
TGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCG
CCCCGGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCAT
ACCATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGCTGCCA
GTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCCCCA
CAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAACAT
ACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAACAATGAACCT
TCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAAGTTCCTGCACCATGACC
AGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATGAAAACTCCCCAGAGATGTGC
CGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAATTGTACGTCCTGGGATGAT
ATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGGAAACCCAGCTGCTGAAGAGACA
ATGAACACCAGCCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGAACACCAGCCCAGGG
ACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCCGGGGACTCCTGCCCCAGCTGCT
GAAGAGACAATGACCACCAGCCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACC
AGCCCCGGGGACTCCTGCCTCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTA
ATTGTGCTTCTGATTGTGTTTGTTGAAAGACTTCACTGTGGAAGAAATTCCTTCCTTACCTG
AAAGGTTTCAGGTAGGCGCTGGCTGAGGGCGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCT
CTGCTGTGTTCCACAGACAGAAACGCCTGC

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FIGURE 300

MARIPKTLKFVVVIVAVLLPVLAISATTARQEEVPQQTVA PQQRHSFKGEECPAGSHRSEHT
GACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSCTMTRDTVCQCKEGTFRNENSPEMCR
KCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGT
PAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLI
VLLIVFV

Important features:**Signal peptide:**

Amino acids 1-29

Transmembrane domain:

Amino acids 240-259

N-glycosylation site:

Amino acids 77-81;140-144;156-160

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 126-130

N-myristoylation sites:

Amino acids 56-62;72-78;114-120;154-160;233-239

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FIGURE 301

CACAAGCATCTTAATTTGAATCCACAAAGTTTCATGTAATGAAAAGAAATACATAATTTTAAT
TCAACCCGAGTGTTTTCCAAGAAGATTGTATTTGCTTAAATTGCTACAGTAATTCAAGAGACA
GCCCTGTCTGGACACAGAGTTACTGTGGATTTTTTAAGAGACTCAGTTAAAGAATTTAGGAATT
TCTGATTCATTTAAAGGATTTACAAATTCATCAACCCCTGAAAACCTAAAGCAAATTGAACAGG
AAAAAAAAAAGAAGATGGGTTTTTTAAGTCCAATATATGTTATTTTCTTCTTTTTTGGAGTC
AAAGTACATTGCCAATATGAACTTATCAGTGGGATGAAGACTATGACCAAGAGCCAGATGAT
GATTACCAAACAGGATTCCCATTTTCGTCAAATGTAGACTACGGAGTTCCTTTTCATCAGTAT
ACTTTAGGCTGTGTCAGTGAATGCTTCTGTCCAACCTAACTTTCCATCATCAATGTACTGTGAT
AATCGCAAACCTCAAGACTATCCCAAATATTCGATGCACATTCAGCAACTCTACCTTCAGTTC
AATGAAATTGAGGCTGTGACTGCAAATTCATTCATCAATGCAACTCATCTTAAAGAAATTAAC
CTCAGCCACAACAAATTAATCTCAAAGATTGATTATGGTGTGTTTGCTAAGCTTCCAAAT
CTACTACAACCTTCATCTAGAGCATAATAATTTAGAAGAATTTCCATTTCTCTTCTTAAATCT
CTGGAAAGACTCCTTCTTGGTTACAATGAAATCTCCAACTGCAGACAAATGCTATGGATGGG
CTAGTAACTTGACCATGCTTGATCTCTGTTATAATTATCTTCATGATTCTCTGCTAAAAGAC
AAAATCTTTGCCAAATGGAAAACTAATGCAGCTCAACCTCTGCAGTAACAGATTAGAATCA
ATGCCTCCTGGTTTGCCTTCTTCACTTATGTATCTGTCTTTAGAAAATAATTCAATTTCTTCT
ATACCCGAAAAATACTTCGACAACTTCCAAACTTCATACTCTAAGAATGTCACACAACAAA
CTACAAGACATCCCATATAATATTTTTAATCTTCCCAACATTGTAGAACTCAGTGTTGGACAC
AACAAATTGAAGCAAGCATTCTATATTCCAAGAAATTTGGAACACCTATACCTACAAAATAAT
GAAATAGAAAAGATGAATCTTACAGTGATGTGTCCTTCTATTGACCCACTACATTACCACCAT
TTAACATACATTTCGTGTGGACCAAATAAACTAAAAGAACCAATAAGCTCATACATCTTCTTC
TGCTTCCCTCATATACACACTATTTATTATGGTGAACAACGAAGCACTAATGGTCAAACAATA
CAACTAAAGACACAAGTTTTTCAGGAGATTTCCAGATGATGATGATGAAAGTGAAGATCACGAT
GATCCTGACAATGCTCATGAGAGCCCAGAACAAGAAGGAGCAGAAGGGCACTTTGACCTTCAT
TATTATGAAAATCAAGAAATAGCAAGAACTATATAGGTATACACTTACGACTTCACAAAACCTA
TACTTAATATAGTAAATCTAAGTAAACATGTATTACTCAAAGTAATATATTTAGAATTATGTA
TTAGTATAAGATCAGAATTGAATTTAAGTTGTTGGTGACATCTGCATCATTTTCATAGGATTAG
AACTTACTCAAATAATGTAAATCTTTAAAATATAAATTAGAATGACAAGTGGGAATCATAA
ATTAAACGTTAATGGTTTCTTATGCTCTTTTTAATATAGAAATATCATGTTAAAGAAAAAA
AAAAAA

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FIGURE 302

MGFLSPIYVIFFFFGVKVHCQYETYQWDEDYDQEPDDDYQTGFPRQNVGYGVPFHQYTLGCV
SECFCPTNFPSSMYCDNRKLKTIPNIPMHIQQLYLQFNEIEAVTANSFINATHLKEINLSHNK
IKSQKIDYGVFAKLPNLLQLHLEHNNLEEFPPPLPKSLERLLLGYNEISKLQTNAMDGLVNLT
MLDLCYNYLHDSLLKDKIFAKMEKLMQLNLCSNRLESMPPGLPSSLMYLSLENNSSIPIKEY
FDKLPKLHTLRMSHNKLQDIPYNIFNLPNIVELSVGHNKLKQAFYIPRNLEHLYLQNNIEKM
NLTVMCPSIDPLHYHHLTYIRVDQNKLEKPISSYIFFCFPHIHTIYYGEQRSTNGQTIQLKTQ
VFRFRPDDDDDESEDHDDPDNAHESPEQEGAEGHFDLHYENQE

Important features:**N-glycosylation sites:**

Amino acids 113-117;121-125; 187-191;242-246;316-320

Tyrosine kinase phosphorylation sites:

Amino acids 268-275;300-307

N-myristoylation site:

Amino acids 230-236

Leucine zipper patterns:

Amino acids 146-168;217-239

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FIGURE 303

GCCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAGC
TGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTACCA
CGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGC**ATGA**ATCTGGT
AGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTATGAT
ACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGGGGTTT
AAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGAAACAGT
CTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGGACCTCCA
TCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCATGCCTTCAA
AGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAGTGTGCACAA
AAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGCACTGCGACTG
TACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCACAACGTGATCTG
TAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGCCAACGACGCTGA
CCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCATGTTTGGCTGGTT
CACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAGGATGCCCCGGAGACA
CCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGAACCTGATGATATTAG
CACTGTGGT**ATAG**TGTCCAACTGACTGTCATTGAGAAAGAAAGAAAGTAGTTTGCGATTGCA
GTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAACTTTGTATTTTCAGTTT
TTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACATAAATAATTTGAGTTTAG
GTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGTAAGCTACTATCTGAACATT
AGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTTAATTTAAAAGCAAATAAAAG
CTTAACTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAAAAAACA

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FIGURE 304

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMCPKGCLCSSSGGLNVTCSNANLKEIPRDL
PETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLSDNRIQ
SVHKNAFNNLKARARIANNPWCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFLNAA
NDADLCNLPKKTDDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKKADEP
DDISTVV

Important features:**Signal sequence:**

Amino acids 1-33

Transmembrane domain:

Amino acids 204-219

N-glycosylation sites:

Amino acids 47-51;94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation sites:

Amino acids 37-43;45-51;110-116

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FIGURE 305

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCCGCTCCTAGTGGTTTTTCCACTTTGTTGAATTGTTCCCT
ATACTCAAATTCACCAAGACACCTTGTCTCCCAAATGCAAAATGTGAAATACGCAATGGAATTGAAGCCTGCT
ATTGCAACATGGGATTTTCAGGAAATGGTGTCACAATTTGTGAAGATGATAATGAATGTGGAAATTTAACTCAGT
CCTGTGGCGAAAATGCTAATTGCACTAACACAGAAGGAAGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCA
GCAGTAACCAAGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATTTAG
ATAATGTCTGTATAGCTGCAATATTAATAAAACTTTAACAAAATCAGATCCATAAAAGAACCTGTGGCTTTGC
TACAAGAAGTCTATAGAAATTCTGTGACAGATCTTTCACCAACAGATATAATTACATATATAGAAATATTAGCTG
AATCATCTTCATTACTAGGTTACAAGAACAACACTATCTCAGCCAAGGACACCCTTTCTAACTCAACTCTTACTG
AATTTGTA AAAACCGTGAATAATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATA
GGAGAACACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCCAAAAGA
CCACAGAGTTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTTTTGTATTACATAACATGAAACATA
TTCATCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGAGAAAAGCTGCATATGATTCAAATG
GCAATGTTGCAGTTGCATTTTTATATTATAAGAGTATTGGTCTTTGCTTTCATCATCTGACAACCTCTTATTGA
AACCTCAAATATGATAATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAA
ACCCACCACATTATATGAACTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATAGGA
GTCTATGTGCATTTTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAGGGCTGTGAGCTGACAT
ACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACATTTTGCATTTTGTATGTCTCTGGTCTCTT
CCATTGGTATTAAAGATTATAATATTCTTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTG
CCATATGCATTTTTACCTTCTGGTTCTTCAGTGAAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCT
GTAGCCTATTTCTTGCTGAACTTGTTTTCTTGTTGGGATCAATACAAATACTAATAAGCTCTTCTGTTCAATCA
TTGCCGGA CTGCTACACTACTTCTTTTAGCTGCTTTTGCATGGATGTGCATTGAAGGCATACATCTCTATCTCA
TTGTTGTGGGTGTCTATCTACAACAAGGGATTTTTGCACAAGAATTTTTATATCTTTGGCTATCTAAGCCCAGCG
TGGTAGTTGGATTTTCGGCAGCACTAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAA
ACAACCTTTATTTGGAGTTTATAGGACCAGCATGCCTAATCATTCTTGTAAATCTCTTGGCTTTTGGAGTCATCA
TATACAAAGTTTTTCGTCACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAACATAAGGTCTTGTGCAA
GAGGAGCCCTCGCTCTTCTGTTCCTTCTCGGCACCACCTGGATCTTTGGGGTCTCCATGTTGTGCACGCATCAG
TGGTTACAGCTTACCTCTTCAGCTCAGCAATGCTTTCCAGGGGATGTTCAATTTTTTATTCTGTGTGTTTTAT
CTAGAAAGATTCAAGAAGAATATTACAGATTGTTCAAAAATGTCCCCTGTTGTTTTGGATGTTTAAGGTTAAACAT
AGAGAATGGTGGATAATTACAACCTGCACAAAATAAAAATTCAGCTGTGGATGACCAATGTATAAAAATGACT
CATCAAATTATCCAATTATTACTACTAGACAAAAGTATTTTAAATCAGTTTTTCTGTTTATGCTATAGGAACT
GTAGATAATAAGGTAAAATTATGTATCATATAGATATACTATGTTTTTCTATGTGAAATAGTTCTGTCAAAAATA
GTATTGCAGATATTTGGAAAGTAATTGGTTTCTCAGGAGTGATATCACTGCACCCAAGGAAAGATTTTCTTTCTA
ACACGAGAAGTATATGAATGTCCTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTGCTTTGAACT
AGTCCCCTACCACCTCGGTAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGGCGAATATCAAA
CAGTGAAGGGAATGATAAGATGATTTTGAATGAAGTGTGTTTTCTGTAGACTAGCTGAGAAATTGTTGACAT
AAAATAAAGAATTGAAGAAACACATTTTACCATTTTGTGAATTGTTCTGAACTTAAATGTCCACTAAAACAACCTT
AGACTTCTGTTTGCTAAATCTGTTTCTTTTCTAATATTCTAAAAAAGGTTTACCTCCACAAATTGA
AA

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FIGURE 306

MKRLPLLVVFSTLLNCSYTNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNECGNLTQSCGENANC
TNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVNANCHLDNVCIAANINKTLTKIRSIKEPVALLQEVYRNS
VTDLSPTDIITYIEILAESSLLGYKNNTISAKDTLSNSTLTEFVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKL
MHTVEQATLRISQSFOKTTEFDTNSTDIALKVFFFDSYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAVAF
YYKSIGPLLSSSDNFFLLKPQNYDNSEEEERVISVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAFWNY
SPDTMNGSWSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLGIIISLICLAICIFTFW
FFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSEIAGLLHYFFLAFAWMCIEGHLVYLVVGVYIN
KGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGTTKVCWLSTENNFWSFIGPACLIILVNLLAFGVIIYKVERHT
AGLKPEVSCFENIRSCARGALALLFLLGTTWIFGVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEY
YRLFKNVPCCFGCLR

Important features:**Signal peptide:**

Amino acids 1-19

Transmembrane domain:

Amino acids 431-450;494-515;573-594;619-636;646-664

N-glycosylation sites:Amino acids 15-19;21-25;64-68;74-78;127-131;177-181;
188-192;249-253;381-385;395-399**Glycosaminoglycan attachment site:**

Amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 360-364

Tyrosine kinase phosphorylation sites:

Amino acids 36-44;670-677

N-myristoylation sites:Amino acids 38-44;50-56;52-58;80-86;382-388;388-394;
434-440;480-486;521-527**Aspartic acid and asparagine hydroxylation site:**

Amino acids 75-87

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FIGURE 307

CCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGT
ATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGGC
CCGGAGGAGCGCCTTCCCTGCCGCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGA
GGCCGGGCCCGCCGAGGAGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGA
AGAAGATATCCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGATTTTCAGAAAAGCGCAACAGAGAAT
GCCAGCTATTCCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGA
ATTCCTGTCTTGCGCTCCCTGGATAAAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGT
GCCTCACAAGGCATCAGTTGTTCAAGTTGGTTTCCCATGTCTTGAAAAACAGGATGGGGTGGCAGCATTTGAAGT
GGATGTGATTGTTATGAATTCGAAGGCAACACCATTCTCCAAACACCTCAAAATGCTATCTTCTTTAAACATG
TCAACAAGCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAAATGAAAGACGCATCTGCGAGTGTCTGA
TGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATGGTGGACTTTGTGTGACTCC
TGGTTTCTGCATCTGCCACCTGGATTCTATGGAGTGAAGTGTGACAAAGCAAAGTCTCAACCACCTGCTTTAA
TGGAGGGACCTGTTTCTACCCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAA
ATGCCCACAACCTGTGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTTCAAAGGTTACCAGGG
AGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCCAACAAATGCCA
ATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGC
AGGCGCCAGCTCAGGCAGCACACGCCTTCACTTAAAAAGGCCGAGGAGCGGGGATCCACCTGAATCCAATTA
CATCTGGTGAACTCCGACATCTGAAACGTTTTAAGTTACACCAAGTTTCATAGCCTTTGTAAACCTTTTCATGTGTT
GAATGTTCAAATAATGTTTATTACCTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGC
TGATATTTACTCTTCCTTTTAAGTTTTCTAAGTACGTCTGTAGCATGATGGTATAGATTTTCTTGTTCAGTGCT
TTGGGACAGATTTTATATTATGTCAATTGATCAGGTTAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAAT
TACAATGCATTTATGGTGTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTGGGCAAAATGCGTAAGTCACAA
GAATTTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAGATTTTATTGTGAGATATTTAGATGTTTGTTAC
ATTTTTAAAAATTGCTCTTAATTTTTAACTCTCAATACAATATATTTTGACCTTACCATTATTCCAGAGATTCA
GTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATTAAACAATATAATATATTCTAAACACAATGAAATAG
GGAATATAATGTATGAACCTTTTGCATTGGCTTGAAGCAATATAATATATTGTAAACAAAACACAGCTCTTACCT
AATAAACATTTTATACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAAAAAAAAAAAAA
AAAAAAA

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FIGURE 308

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGKM
APFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEIFYEFSLRSLDKGIMADPTVNVPLLGT
VPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGCRNG
GFCNERRICECPDGFHGHPCHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCSTTCFN
GGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCKGKCKSKGYQGDLCSPVCEPGCG
AHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEEERRDPPESNYIW

Important features:**Signal sequence:**

Amino acids 1-28

N-glycosylation sites:

Amino acids 88-92;245-249

Tyrosine kinase phosphorylation site:

Amino acids 370-378

N-myristoylation sites:

Amino acids 184-190;185-191;189-195;315-321

ATP/GTP-binding site motif A (P-loop):

Amino acids 285-293

EGF-like domain cysteine pattern signatures:

Amino acids 198-210;230-242;262-274;294-306;326-338

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FIGURE 309

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCTGCGCACAGATGCGGG
TTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGACT
CTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATGGAG
ATGGATTTCTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTGGCCG
TGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTTCGATG
ACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCGAGCGGAGGGG
TTTTCTTTGAAGGCTCTGTAGCCCGATTCTACTGCCAAGACGGATTCAAGCTGAAGGGCGCTA
CAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGATAATTCCA
TCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTTCATAACAAGACAT
ATAGACATGGAGAGAAGCTAATCATCACTTGTATGAAGGATTCAAGATCCGGTACCCCGACC
TACACAATATGGTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGCCCATCTGTCAAG
GCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGCTCCAGACCTCCT
TCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTTGATGGGTCTGCGT
ATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGGTGCCTTGCTCTGGAAG
CCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGCTGCCACCCGCGGCCTT
GTGAGCGCTACAACCACGGAACGTGTGGTGGAGTTTTACTGCGATCCTGGCTACAGCCTCACCA
GCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTCTTATCAAGTCTACTGCA
TCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCCCTCCTGACCACGTGGAAGATTGTGG
CGTTCACGGCAACCAGTGTGCTGCTGGTGCTGCTCGTCATCCTGGCCAGGATGTTCCAGA
CCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAGTTCCAGCAGTGACCCTGACT
TTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCTATGACGAAGCTGTGAGTGCGCGCT
TGAGTGCCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAGGGCTGCCCCTTACCCGTGGACG
ACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGACACAGGCCCAGGGGAGTCAGAAA
CCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAAGTCTGTATTACCTCCCAGGTGCC
AAGAGAGCACCCACCCTGCTTCGGACAACCCTGACATAATTGCCAGCACGGCAGAGGAGGTGG
CATCCACCAGCCCAGGCATCCATCATGCCCACTGGGTGTTGTTCCCTAAGAAACTGATTGATTA
AAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAAATACATGTTGATCTGTGGAGTTGATTC
CTTTCCTTCTCTTGGTTTTAGACAAATGTAAACAAAGCTCTGATCCTTAAAATTGCTATGCTG
ATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTCCTGTTTCTTCTTGACACAGACTGATTAAA
AATTAAAAGNAAAAA

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FIGURE 310

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLAVILWFQLALCFGPAQLTGGFDDLQVCADPGIP
ENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRIPQ
IEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLASSNG
YVNISELQTSFPVGTVISYRCFPFGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLPPMV
HGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQTWPSTH
ETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVDGVPVML
PSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDSVSGSSEL
LQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVFLRN

Important features:**Signal sequence:**

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472**N-myristoylation site.**amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

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FIGURE 311

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGC**ATG**AGCGGCGGTTGGATGGCGCAGGTTGGAG
CGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCTGG
AGGCCGCCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGCGAGGCCCCAGCTCAGGCT
CGTGCCCAACCAAGTTCCAGTGCCGCACCAAGTGGCTTATGCGTGCCCTCACCTGGCGCT
GCGACAGGGACTTGGA^{CT}GCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCCATGTA
CCCAGAAAGGGCAATGCCCACCGCCCCCTGGCCTCCCCTGCCCCCTGCACCGGCGTCAGTGA^{CT}
GCTCTGGGGGA^{CT}GTACAAGAA^{CT}TGCGCA^{CT}TGCAGCCGCCTGGCCTGCCTAGCAGGCGAGC
TCCGTTGCACGCTGAGCGATGACTGCATTCCA^{CT}CACGTGGCGCTGCGACGGCCACCCAGACT
GTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAGGGGATGCCA
CAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCA^{CT}CTCTCAGGAATGCCACAACCATGG
GGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTCCTCTGCCGGAG
ACCAGTCTGGAAGCCCA^{CT}TGCCTATGGGGTTATTGCAGCTGCTGCGGTGCTCAGTGCAAGCC
TGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGCCTCCGCCCAC^{CT}TGG
GGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGACCTCGCTGCCCT**TGAG**
GACAAGCACTTGCCACCACCGTCA^{CT}CTCAGCCCTGGGCGTAGCCGGACAGGAGGAGAGCAGTGA
TGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTTCTGGCCACGTGGAACC
TCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCCTGGACACTCCCTATGGA
GATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAGGGGCTGGCCCCAGGCAGC
TCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTGCCCCGTCTGAGGGTGGCGA
TTAAAGTTGCTTC

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FIGURE 312

MSGGWMAQVGAWRTGALGLALLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRT
SGLCVPLTWRCRDLDCSDGSDEEECRIEPC TQKGQC PPPPG L P C P C T G V S D C S G G T D K K L R N
CSRLACLAGE LRCTLSDDCIPLTWRC D G H P D C P D S S D E L G C G T N E I L P E G D A T T M G P P V T L E S
VTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLV TAT L L L L S W
LRAQERLRPLG L L V A M K E S L L L S E Q K T S L P

Important features:**Signal sequence:**

Amino acids 1-30

Transmembrane domain:

Amino acids 231-248

N-glycosylation sites:

Amino acids 126-130;195-199;213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation sites:Amino acids 3-9;10-16;26-32;30-36;112-118;166-172;212-218;
224-230;230-236;263-269**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 44-55

Leucine zipper pattern:

Amino acids 17-39

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FIGURE 313

CGGACGCGTGGGCGTCCGGCGGTTCGCAGAGCCAGGAGGCGGAGGCGCGGGCCAGCCTGGGCCCCAGCCCACAC
CTTCACCAGGGCCCAGGAGCCACCATGTGGGCGATGTCCACTGGGGCTACTGCTGTTGCTGCCGCTGGCTGGCCAC
TTGGCTCTGGGTGCCAGCAGGGTCTGTGGGCGCCGGGAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGAC
GCGGGAGGCCGGTACTGCCAGGAGCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTG
GGCGCCATCTGTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTCTGC
CTCGGCGTGCCACCCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTATCCAGTCTTGGGAACG
TACTGGGACAACCTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGTGGCATGGTGGATCCAGACATGATCAAAGC
CATCAACCAGGGCAACTATGGCTGGCAGGCTGGGAACCACAGCGCCTTCTGGGGCATGACCCTGGATTGAGGGGCAT
TCGCTACCGCCTGGGCACCATCCGCCCATCTTCCTCGGTTCATGAACATGCATGAAATTTATACAGTGCTGAACCC
AGGGGAGGTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGACCAAGG
CAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCTCAATCCATTCTCTGGGACA
CATGACGCCTGTCCTGTGCCCCAGAACCTGCTGTCTTGTGACACCCACCAGCAGCAGGGCTGCCGCGGTGGGCG
TCTCGATGGTGCCTGGTGGTTTCTGCGTCGCCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGA
ACGAGACGAGGCTGGCCCTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCAC
TGCCCCACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTCCAA
CGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGGTGCATGAGGACTTCTT
CCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGGAGGCCAGAGAGATACCGCCGGCATGGGAC
CCACTCAGTCAAGATCACAGGATGGGGAGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGC
CAACTCCTGGGGCCCCAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGC GCGGCGTCAATGAGTGCGACATCGA
GAGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCATCACTGAGGCTGCGGGCACCACGC
GGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATGGGGCGGTGACCCCAGCCTCGCCGA
CAGAGCCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAATCCCGGCGGGGTTCGCTGACGCAGCGCCCCGCCTGGG
AGCCGCGGGCAGGCGAGACTGGCGGAGCCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAG
CACAGCTGCAGATCCCAGGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGCCC
CAATACCCCACCCAATCCCGTATTCTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCGTTGCCAGGTTGGAG
TGCAGTGGCCCATCAGGGTCACTGTAACCTCCGACTCCTGGGTTCAAGTGACCCTCCCACCTCAGCCTCTCAAG
TAGCTGGGACTACAGGTGCACCACCACACCTGGCTAATTTTTGTATTTTTTGTAAGAGGGGGGTCTCACTGTGT
TGCCCAGGCTGGTTTCGAACTCCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGCTGGGATTGCAGG
CATGAGCCACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAATAAAA
CCAAAGTATTGATAAAAAAAAAA

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FIGURE 314

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDCA
LPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNRCT
CQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

Important features:**N-glycosylation site.**

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

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FIGURE 315

CGGACGCGTGGGCCCCCTGGTGGGCCCAGCAAGATGGATCTACTGTGGATCCTGCCCTCCCTGT
GGCTTCTCCTGCTTGGGGGGCCTGCCTGCCTGAAGACCCAGGAACACCCCAGCTGCCCAGGAC
CCAGGGAACTGGAAGCCAGCAAAGTTGTCCTCCTGCCCAGTTGTCCCGGAGCTCCAGGAAGTC
CTGGGGAGAAGGGAGCCCCAGGTCCTCAAGGGCCACCTGGACCACCAGGCAAGATGGGCCCCA
AGGGTGAGCCAGGCCCCAGAACTGCCGGGAGCTGTTGAGCCAGGGCGCCACCTTGAGCGGCT
GGTACCATCTGTGCCTACCTGAGGGCAGGGCCCTCCCAGTCTTTTGTGACATGGACACCGAGG
GGGGCGGCTGGCTGGTGTTCAGAGGCGCCAGGATGGTTCTGTGGATTTCTTCCGCTCTTGGT
CCTCCTACAGAGCAGGTTTTTGGGAACCAAGAGTCTGAATTCTGGCTGGGAAATGAGAATTTGC
ACCAGCTTACTCTCCAGGGTAAGTGGGAGCTGCCGGTAGAGCTGGAAGACTTTAATGGTAACC
GTACTTTCGCCCCTATGCGACCTTCCGCCTCCTCGGTGAGGTAGACCACTACCAGCTGGCAC
TGGGCAAGTTCTCAGAGGGCACTGCAGGGGATTCCCTGAGCCTCCACAGTGGGAGGCCCTTTA
CCACCTATGACGCTGACCACGATTCAAGCAACAGCAACTGTGCAGTGATTGTCCACGGTGCCT
GGTGGTATGCATCCTGTTACCGATCAAATCTCAATGGTCGCTATGCAGTGTCTGAGGCTGCCG
CCCACAAATATGGCATTGACTGGGCCTCAGGCCGTGGTGTGGGCCACCCCTACCGCAGGGTTC
GGATGATGCTTCGATTAGGGCACTCTGGCAGCCAGTGCCCTTATCTCTCCTGTACAGCTTCCGG
ATCGTCAGCCACCTTGCCTTTGCCAACCACCTCTGCTTGCCTGTCCACATTTAAAAATAAAAT
CATTTTAGCCCTTTCA

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FIGURE 316

MDLLWILPSLWLLLLGGPACLKTQEHPSCPGPRELEASKVVLLPSCPGAPGSPGEKGAPGPQG
PPGPPGKMGPKGEPGPRNCRELLSQGATLSGWYHLCLPEGRALPVFCMDMTEGGGWLVFQRRQ
DGSVDFFRSWSSYRAGFGNQESEFWLGNENLHQLTLQGNWELRVELEDFNGNRTFAHYATFRL
LGEVDHYQLALGKFSEGTAGDSLHSGRPFTTYDADHDSSNSNCAVIVHGAWWYASCYRSNL
NGRYAVSEAAAHKYGIDWASGRGVGHPYRRVRMMLR

Important features:**Signal peptide:**

Amino acids 1-16

N-glycosylation site:

Amino acids 178-182

Glycosaminoglycan attachment site:

Amino acids 272-276

Tyrosine kinase phosphorylation site:

Amino acids 188-197

N-myristoylation sites:

Amino acids 16-22;89-95;144-150;267-273

Fibrinogen beta and gamma chains C-terminal domain signature:

Amino acids 242-255

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FIGURE 317

CCCAAGCCAGCCGAGCCGCCAGAGCCGCGGGCCGCGGGGGTGTGCGGGGCCCAACCCCAGGAT
GCTCCCCTGCGCCTCCTGCCTACCCGGGTCTCTACTGCTCTGGGCGCTGCTACTGTTGCTCTT
GGGATCAGCTTCTCCTCAGGATTCTGAAGAGCCCGACAGCTACACGGAATGCACAGATGGCTA
TGAGTGGGACCCAGACAGCCAGCACTGCCGGGATGTCAACGAGTGTCTGACCATCCCTGAGGC
CTGCAAGGGGGAAATGAAGTGCATCAACCACTACGGGGGCTACTTGTGCCTGCCCCGCTCCGC
TGCCGTCATCAACGACCTACATGGCGAGGGACCCCCGCCACCAGTGCCTCCCGCTCAACACCC
CAACCCCTGCCACCAAGGCTATGAGCCCGACGATCAGGACAGCTGTGTGGATGTGGACGAGTG
TGCCAGAGGCCCTGCACGACTGTGCCCCAGCCAGGACTGCCATAACTTGCCTGGCTCCTATCA
GTGCACCTGCCCTGATGGTTACCGCAAGATCGGGCCCCGAGTGTGTGGACATAGACGAGTGCCG
CTACCGCTACTGCCAGCACCGCTGCGTGAACCTGCCTGGCTCCTTCCGCTGCCAGTGCAGGCC
GGGCTTCCAGCTGGGGCCTAACAACCGCTCCTGTGTTGATGTGAACGAGTGTGACATGGGGGC
CCCATGCGAGCAGCGCTGCTTCAACTCCTATGGGACCTTCTGTGTCGCTGCCACCAGGGCTA
TGAGCTGCATCGGGATGGCTTCTCCTGCAGTGATATTGATGAGTGTAGCTACTCCAGCTACCT
CTGTCAGTACCGCTGCGTCAACGAGCCAGGCCGTTTCTCCTGCCACTGCCCCACAGGGTTACCA
GCTGCTGGCCACACGCCTCTGCCAAGACATTGATGAGTGTGAGTCTGGTGCGCACCAAGTGTCTC
CGAGGCCCAAACCTGTGTCAACTTCCATGGGGGCTACCGCTGCGTGGACACCAACCGCTGCGT
GGAGCCCTACATCCAGGTCTCTGAGAACCGCTGTCTCTGCCCGGCCTCCAACCTCTATGTCTG
AGAGCAGCCTTCATCCATTGTGCACCGCTACATGACCATCACCTCGGAGCGGAGCGTGCCCCG
TGACGTGTTCCAGATCCAGGCGACCTCCGTCTACCCCGGTGCCTACAATGCCTTTCAGATCCG
TGCTGGAAACTCGCAGGGGGGACTTTTACATTAGGCAAATCAACAACGTCAGCGCCATGCTGGT
CCTCGCCCCGGCCGGTGACGGGGCCCCCGGGAGTACGTGCTGGACCTGGAGATGGTCACCATGAA
TTCCCTCATGAGCTACCGGGCCAGCTCTGTACTGAGGCTCACCGTCTTTGTAGGGGCCTACAC
CTTCTGAAGGAGCAGGAGGGAGCCACCCTCCCTGCAGCTACCCTAGCTGAGGAGCCTGTTGTGA
GGGGCAGAATGAGAAAGGCAATAAAGGGAGAAAGAAAGTCTGGTGGCTGAGGTGGGCGGGTC
ACACTGCAGGAAGCCTCAGGCTGGGGCAGGGTGGCACTTGGGGGGGCGAGGCCAAGTTCACCTA
AATGGGGGTCTCTATATGTTTCAGGCCCGAGGGGCCCCCATTGACAGGAGCTGGGAGCTCTGCAC
CACGAGCTTCAGTCACCCCGAGAGGAGAGGAGGTAACGAGGAGGGCGGACTCCAGGCCCCGGC
CCAGAGATTTGGAATTGGCTGGCTTGCAGGGGTCCTAAGAACTCCACTCTGGACAGCGCCAG
GAGGCCCTGGGTTCATTCTAACTCTGCCTCAAACGTACATTTGGATAAGCCCTAGTAGTT
CCCTGGGCCTGTTTTTCTATAAAACGAGGCAACTGGAAAAAAAAAAAAA

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FIGURE 318

MLPCASCLPGSLLLWALLLLLLLGSASPQDSEEPDSYTECTDGYEWD PDSQHCRDVNECLTIPE
ACKGEMKCINHYGGYLCLPRSAAVINDLHGEGPPPPVPPAQHPNPPCPGYEPDDQDSCVDVDE
CAQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCE
PGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQGYELHRDGFSCSDIDECSSYSSY
LCQYRCVNEPGRFSCHCPQGYQLLATRLCQDIDECESGAHQCEAQTCVNFHGGYRCVDTNRC
VEPYIQVSENRCCLCPASNPLCREQPSSIVHRYMTITSESVPADVFQIQATSVYPGAYNAFQI
RAGNSQGDFYIRQINNVSAMLVLARPVTGPREYVLDLEMVTMNSLMSYRASSVLRLTVFVGAYTF

Important features:**Signal sequence:**

Amino acids 1-25

N-glycosylation sites:

Amino acids 198-202;394-398

N-myristoylation sites:Amino acids 76-82;145-151;182-188;222-228;290-296;305-311;
371-377;381-387**Aspartic acid and asparagine hydroxylation sites:**

amino acids 140-152;177-189;217-229;258-270

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FIGURE 319

GCTGGGGAC**ATG**AGAGGGCACACCGAAGACCCACCTCCTGGCCTTCTCCCTCCTCTGCCTCCTC
TCAAAGGTGCGTACCCAGCTGTGCCCCGACACCATGTACCTGCCCCTGGCCACCTCCCCGATGC
CCGCTGGGAGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGCCGGGTATGTGCACGGCGGGCTG
GGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGCCAGGGCCTGGTCTGCCAGCCCGGG
GCAGGACCCGGTGGCCGGGGGGCCCTGTGCCTCTTGGCAGAGGACGACAGCAGCTGTGAGGTG
AACGGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCAGCATCCGCTGCCGCTGC
GAGGACGGCGGCTTCACCTGCGTGCCGCTGTGCAGCGAGGATGTGCGGCTGCCCAGCTGGGAC
TGCCCCCACCACAGGAGGGTCGAGGTCCTGGGCAAGTGCTGCCCTGAGTGGGTGTGCGGCCAA
GGAGGGGGACTGGGGACCCAGCCCCTTCCAGCCCAAGGACCCCAAGTTTCTGGCCTTGTCTCT
TCCCTGCCCCCTGGTGTCCCCTGCCCAGAATGGAGCACGGCCTGGGGACCCTGCTCGACCACC
TGTGGGCTGGGCATGGCCACCCGGGTGTCCAACCAGAACCGCTTCTGCCGACTGGAGACCCAG
CGCCGCCTGTGCCTGTCCAGGCCCTGCCACCCCTCCAGGGGTGCGAGTCCACAAAACAGTGCC
TTCT**TAG**AGCCGGGCTGGGAATGGGGACACGGTGTCCACCATCCCCAGCTGGTGGCCCTGTGCC
TGGGCCCTGGGCTGATGGAAGATGGTCCGTGCCCAGGCCCTTGGCTGCAGGCAACACTTTAGC
TTGGGTCCACCATGCAGAACACCAATATTAACACGCTGCCTGGTCTGTCTGGATCCCGAGGTA
TGGCAGAGGTGCAAGACCTAGTCCCCTTTCCTCTAACTCACTGCCTAGGAGGCTGGCCAAGGT
GTCCAGGGTCCTCTAGCCCACTCCCTGCCTACACACACAGCCTATATCAAACATGCACACGGG
CGAGCTTTCTCTCCGACTTCCCCTGGGCAAGAGATGGGACAAGCAGTCCCTTAATATTGAGGC
TGCAGCAGGTGCTGGGCTGGACTGGCCATTTTTCTGGGGGTAGGATGAAGAGAAGGCACACAG
AGATTCTGGATCTCCTGCTGCCTTTTTCTGGAGTTTGTAATAATTGTTCTGAATACAAGCCTAT
GCGTGA

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FIGURE 320

MRGTPKTHLLAFSLCLLSKVRTQLCPTPCTCPWPPPRCPLGVPLVLDGCGCCRVCAARRLGEP
CDQLHVCDASQGLVCQPGAGPGGRGALCLLAEDDSSCEVNGRLYREGETFQPHCSIRCRCEG
GFTCVPLCSEDVRLPSWDCPHPRRVEVLGKCCPEWVCGQGGGLGTQPLPAQGPQFSGLVSSLP
PGVPCPEWSTAWGPCSTTCGLGMATRVSNQNRFCRLETQRRCLCLSRPCPPSRGRSPQNSAF

Important features:

Signal sequence:

Amino acids 1-23

N-myristoylation sites:

Amino acids 3-9;49-55;81-87;85-91;126-132;164-170;166-172;

167-173;183-189;209-215

Insulin-like growth factor binding proteins signature:

Amino acids 49-65

von Willebrand C1 domain:

Amino acids 107-124

Thrombospondin 1 Homology Block:

Amino acids 201-216

IGF binding protein site:

Amino acids 49-58

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FIGURE 321

AGAACCTCAGAAATGTGAGTTATTTGGAATGGCTGTTTGTAATGTCCTTACGTAAGCCAAG
AGGAGGTCTTGACTTGGGGTCCCAGGGGTACCGCAGATCCCAGGGACTGGAGCAGCACTAGCA
AGTCTGAGGATGAGCCAGGAGTCTGGAATTGAGGCTGAGCCAAAGACCCCAGGGCCGTCTC
AGTCTCATAAAAGGGGATCAGGCAGGAGGAGTTTGGGAGAAACCTGAGAAGGGCCTGATTTGC
AGCATCATGATGGGCCTCTCCTTGGCCTCTGCTGTGCTCCTGGCCTCCCTCCTGAGTCTCCAC
CTTGGAAGTGCCACACGTGGGAGTGACATATCCAAGACCTGCTGCTTCCAATACAGCCACAAG
CCCCTTCCCTGGACCTGGGTGCGAAGCTATGAATTCACCAGTAACAGCTGCTCCCAGCGGGCT
GTGATATTCACTACCAAAGAGGCAAGAAAGTCTGTACCCATCCAAGGAAAAAATGGGTGCAA
AAATACATTTCTTTACTGAAAACCTCCGAAACAATTGTGACTCAGCTGAATTTTCATCCGAGGA
CGCTTGGACCCCGCTCTTGGCTCTGCAGCCCTCTGGGGAGCCTGCGGAATCTTTTCTGAAGGC
TACATGGACCCGCTGGGGAGGAGAGGGTGTTTCCTCCCAGAGTTACTTTAATAAAGGTTGTTC
ATAGAGTTGAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 322

MMGLSLASAVLLASLLSLHLGTATRGSDISKTC CFQYSHKPLPWTWVRSYEFTSNSCSQRAVI
FTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

Important features:

Signal peptide:

amino acids 1-23

N-myristoylation sites.

amino acids 3-9, 26-32

Amidation site.

amino acids 68-72

Small cytokines (intecrine/chemokine).

amino acids 23-88

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FIGURE 323

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGGGGCGTGAGGAGCA
TGCCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGGTGGGCTCAGTGCTGTCAGGCTCGGCCA
CGGGCTGCCCCGCCCCGCTGCGAGTGCTCCGCCCAGGACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAG
TCCCCGAGGGCATCCCCACCGAGACGCGCCTGCTGGACCTAGGCAAGAACC GCATCAAAACGCTCAACCAGGACG
AGTTCGCCAGCTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCCGGCGCCT
TCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATCCCCGCTAGGCGTCTTCA
CTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAAGATCGTTATCCTACTGGACTACATGTTTCAGG
ACCTGTACAACCTCAAGTCACTGGAGGTTGGCGACAATGACCTCGTCTACATCTCTACCGCGCCTTCAGCGGCC
TCAACAGCCTGGAGCAGCTGACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCCACCTGC
ACGGCCTCATCGTCCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGCTGTACC
GACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAACTGCCTCTACGGCCTCAACC
TGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCCCTACCTGGCCGTCCGCCACCTAGTCTATCTCC
GCTTCCTCAACCTCTCCTACAACCCCATCAGCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGG
AGATCCAGCTGGTGGGCGGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGC
TCAATGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGGAGACACTCA
TCCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCGGGCGCCGCTGGCGGGCTCAACTTCA
ACGGGCAGCAGCCCACGTGCGCCACGCCCCGAGTTTGTCCAGGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTAC
TGCCCCAACTACTTCACCTGCCGCCGCGCCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCC
ACACGGTGACGTTTGTGTGCCGGGCGGATGGCGACCCGCGCCCGCCATCCTCTGGCTCTACCCCCGAAAGCACC
TGGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCTACGCCCAGGTAC
AGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGACTCCATGCCCCGCCACCTGCATGTGC
GCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAAGACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAG
AGGCCAACAGCACCCGCGCCACTGTGCCTTTCCCTTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCT
TCATCTCTTTCCCTGGGCGTCGTCCTCTTCTGCCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACACAA
AGCACAAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCGAGGCATCAGCTCCGCCGACGCGCCCCGCAAGT
TCAACATGAAGATGATATGAAGGCCGGGGCGGGGGCAGGGAACCCCGGGCGGCCGGGCGAGGGGAAGGGGCGTGGT
CGCCACCTGCTCACTCTCCAGTCCTTCCACCTCCTCCCTACCCTTCTACACACGTTCTCTTTCTCCCTCCCGCC
TCCGTCCCCTGCTGCCCCCGCCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGG
GGACCCACCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCAATAAT
TCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGGTTTCAATAATTATGGATTTTTATGAAAACCTTGAAATAA
TAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 324

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRRKCFVAVPEGIPTETRL
LDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFFNNLFNLRTLGLRSNRLKLIPLGVFTGLSNLTQDI
SENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRAFSGLSLEQLTLEKCNLTSTPTEALSHLHGLIVLRRLHL
NINAIRDYSFKRLYRLKVLEISHWPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPIS
TIEGSMHELLRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHHSVGNLETILDSNPLACDC
RLLWVFRRRWRLNFNROQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQVFVDEGHTVQFVCRADG
DPPPAIWLSPRKHLVSAKSNGRILTVPDGTLEVRYAQVQDNGTYLCIAANAGGNDSPAHLHVRSYSPDWPHQP
NKTFAFISNQPGEGEANSTRATVPFPFDIKTLIIATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPR
KSDAGISSADAPRKFNMKMI

Important features:**Signal sequence:**

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345, 492-496,
505-509, 526-530, 542-546**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353, 607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143, 262-268, 320-326,
344-350, 359-365, 493-499, 503-509, 605-611**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

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FIGURE 325

CCCACGCGTCCGCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGAG
GCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGAGG
AGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAGGAG
GAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAACGGAG
AGGAGGTGTGGGTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGAGTAGG
AAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGGAAAGAC
ACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTGGCTGCTT
TGGCATTGTTGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCTGGAGGGAC
AGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCAGGGCGTTGGGCAGGGGTCC
CTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCTCGAGCGCTGGTACTC
TGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGGACTGGTGGAGC
TACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGCCTGGTGAATGCA
GCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGAGCTGAAGAGGGTT
CTTTATGACCCCTTTCTGCCCCATTAAAGGCTCAGCACTGGAGGAGAGAAGCTCCGGGGAACC
TTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCTGTGGTCAATGTGTCT
GGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGCAGGCTGCTGTTTGGAGCTCGCGAC
GGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTGAGGTGCAGCTCATTAC
TTCAACCAGGAAGTCTACGGGAATTTACAGCGCTGCCTCCCGCGGCCCCAATGGCCTGGCCATT
CTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCTCCTCAGTCGCCTCCTTAACCGC
GACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTCTTCAAGACCTGAGCCTGGAG
CTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGCTCTCTCAGCACCCCGCCCTGC
TCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAATATCACCTCCCTTCAGATGCAC
TCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCTTCCAGAGCCTCAGCGGTAACAGC
CGGCCCCCTGCAGCCCTTGGCCCACAGGGCACTGAGGGGCAACAGGGACCCCGGCACCCCGAG
AGGCGCTGCCGAGGCCCCAACTACCGCCTGCATGTGGATGGTGTCCCCCATGGTCTGAGAC
TCCCCTTCGAGGATTGCACCCGCCCGTCCTAAGCCTCCCCACAAGGCGAGGGGAGTTACCCCT
AAAACAAAGCTATTAAAGGGACAGAATACTTA

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FIGURE 326

MGAAARLSAPRALVLWAAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCA
VGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLY
SHRLSELRLFLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSLFVN
VASTSNPFLSRLLNRTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSETVTW
ILIDRALNITSLQMHSRLLSQNPPSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPERRCRGP
NYRLHVDGVPHGR

Important features:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 177-199

N-glycosylation sites:

Amino acids 118-122;170-174;260-264

Eukaryotic-type carbonic anhydrases proteins:

Amino acids 222-271;128-165;45-93

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FIGURE 327

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGTGTTGAAGGGTGT
TTTTTCTTTTAAATGTAATACCTCCTCATCTTTTCTTCTTACACAGTGTCTGAGAACATTTACATTATAGATAA
GTAGTACATGGTGGATAACTTCTACTTTTAGGAGGACTACTCTCTTCTGACAGTCCTAGACTGGTCTTCTACACT
AAGACACCATGAAGGAGTATGTGCTCCTATTATTCTGGCTTTGTGCTCTGCCAAACCCCTTCTTTAGCCCTTCAC
ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATGATG
ATGATGATGAGGACAACCTCTCTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTTCCATTGATCTGTTTCCAA
TGTGTCCATTTGGATGTCAGTGCTATTACGAGTTGTACATTGCTCAGATTTAGGTTTGACCTCAGTCCCAACCA
ACATTCATTTGATACTCGAATGCTTGATCTTCAAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAG
GACTCACTTCACCTTTATGGTCTGATCCTGAACAACAACAAGCTAACGAAGATTACCCAAAAGCCTTTCTAACCA
CAAAGAAGTTGCGAAGGCTGTATCTGTCCCACAATCAACTAAGTGAAATACCACCTTAATCTTCCCAATCATTAG
CAGAACTCAGAATTCATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTACACG
TTTTGGAAATGAGTGCAAACCCCTCTTGATAATAATGGGATAGAGCCAGGGGCATTTGAAGGGGTGACGGTGTTC
ATATCAGAATTGCAGAAGCAAACTGACCTCAGTTCTTAAAGGCTTACCACCAACTTTATTGGAGCTTCACCTAG
ATTATAATAAAATTTCAACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCTAGGAA
ACAACAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATTTGGAAAACA
ATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATAATCTTCCCTTCATTCTAATTCAA
TTGCAAGAGTGAGGAGTAAATGACTTCTGTCCAACAGTGCCAAAGATGAAGAAATCTTTATACAGTGCAATAAGTT
TATTCAACAACCCGGTGAAATACTGGGAAATGCAACCTGCAACATTTCTGTTGTGTTTTGAGCAGAATGAGTGTC
AGCTTGGGAACCTTTGGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACAT
TTGGAATACTTGAACTCTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCAAGTGGAAGTCC
ACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAAACTATTGATACATAAGGGGTTGAGAGAAACA
AGCATCTATTGCAGTTTCCTTTTGGCTACAAATGATCTTACATAAATCTCATGCTTGACCATTCCCTTCTTCAT
AACAAAAAGTAAGATATTCGGTATTTAACACTTTGTTATCAAGCACATTTTAAAAGAACTGTAAGTAAATGG
AATGCTTGACTTAGCAAAATTTGTGCTCTTTCATTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGTGA
AGAGTGCATTACACTATTCTTATTCTTTAGTAACCTGGGTAGTACTGTAATATTTTAAATCATCTTAAAGTATGA
TTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGTCTTTATGTTTAAACTAATTTCTTAAAA
TAAAGCCTTCAGTAAATGTTTATTACCAACTTGATAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATAT
GCTTTTTTTTTTTAATTATTACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAAC
CGCATTTTAAATGATCCGCTATTATAAGCTTTTAAATAGCATGAAAATGTTAGGCTATATAACATTGCCACTTCAA
CTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGCTTGGAAGAGCCTGGACACTAACAAATCTACACC
AAATTGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAACACATCTAGTATAACTGAATAAGCAGAGCAT
CAAATTAAACAGACAGAAACCGAAAGCTCTATATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCAA
CATATGTAAATCAGAAACAGGGAAATTTTCATTAAAAATATTGGTTTGAAT

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FIGURE 328

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDEDNSLFPTREPRS
HFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTS
LYGLILNNKLTKEIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDT
FKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI
STVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKCLKKIPSGLPPELKYLQI
IFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQLGNFGM

Important features:**Signal sequence.**

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

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FIGURE 329

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGCA
TCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGTGT
TTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGTGTT
CAGCATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACCAGCG
GCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGCCTGCT
GAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCCGCTCCC
GCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAACCTCAGTTTGA
TTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCTCAATACCA
TGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCATGCAGCAAAT
GTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTCTTTCACCAAC
CTTCAACCCACAGGAGGTCTTTATTCTGTTCCACTAACATTTTTTCGGAATCTGGAGTCCACCCG
TTGTTTGCTGGCTGGGCTTTTCCAGTGTCAGAAAGAAGGACCCATCATCATCCACACTGATGA
AGCAGATTGAGAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGAGGCAGAGAACCAG
AGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTGAAAAAGGTGAAGGA
CAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCTGGACAACGTGGCTGC
CGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTGCACGGATGATCGAACA
GAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGGGAAAGTCTTCAGATGGC
AGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGCCATGGACTCTGCCACTGC
CCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATGTGACCTTCATACCGCTCTT
AATGACCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCTGTTGACCTGACCATGGAAC
TTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTATTACCACGGGAAGGAGCAGGT
GCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGTTCTTGAATGCCATGTCAGTTTA
TACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAAACCTCAGGTGATGGAAGTTGGAAA
TGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATTTTAAATAAAGTGCCTTTATACAATG

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FIGURE 330

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMQVVFRHGARSPLKPLPLEEQVE
WNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFALGERLRKNYVEDIPFL
SPTFNPQEVFIRTNIFRNLESTRCLLAGLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTGRRTASLQ
PGISEDLLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMA
VGPFLHILESNNLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEWFVQ
LYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

Important features:**Signal sequence:**

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

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FIGURE 331

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACATTTTTCCCTTTCCT
AACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTTGCTGGAGAAGAAAGGGCTGAGGGCAG
AGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTGCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGAT
GCAGCGGAGTGAGGTGATGGAAGTCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGA
CCTGGAGAGCCTGGGGGAGGGCCTGCCTAACAAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGATAAG
ACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCTTAATATCAAATTGACTGGCTGGGTGAACCTCAACAGCCT
TTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAATAGAGATGCTTTGTAAATAAAATTTTAA
AAAAAGCAAGTATTTTATAGCATAAAGGCTAGAGACCAAATAGATAACAGGATTCCCTGAACATTCTAAGAGG
GAGAAAGTATGTTAAAAATAGAAAAACCAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGGACC
CTGGGTGAGGCCAGCCTCTTGCTCCTCCCGAAATTATTTTTGGTCTGACCACTCTGCCTTGTGTTTTGCAGAA
TCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCTCCTCACCGCCGCCCTCTC
AGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGGACAGCCGCTCTGTGGTCTGCTCTCAGTGGTC
TGGGTGCTGCTGGCCCCCCCCAGCAGCCGGCATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACC
TTCAACCACTTGACCGTCCACCAAGGGACGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACA
GGCAACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCGCCCTCATC
GTGCAGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAGCTGCTCATCATTGACTACTCTGAGAAC
CGCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCAAGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTG
GAGCCATCCCACAAGAAGGAGCACTACCTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGC
TCTGAGGGTGAGGATGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCC
AGCCGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGATTTTGTCTCCTCT
CTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACATCTTCTACATCTACGGCTTTGCTAGT
GGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCAGACCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTC
TTCTACACCTCACGCATCGTGCGGCTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGC
TGACCCGGGCGGGGGTGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCCAG
GCCTTCAATATACACAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAGCAGTATCACACCCG
CCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTTGCAGATCAAGGAGCGCTGCAGTCTGC
TACCAGGGCGAGGGCAACCTGGAGCTCAACTGGCTGCTGGGGAAGGACGTCCAGTGACGAAGGCGCCTGTCCCC
ATCGATGATAACTTCTGTGGACTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGTGAGGGCCTGACCCTG
TACACCACCAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTGTGGGG
ACTAAGAGTGGAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCCATTACCTCCTCAGCAAA
GAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAGGCAACTTTATTTTCTTGGGGAACAAAGGTGA
AATGGGGAGGTAAGAAGGGGTAAATTTGTGACTTAGCTTCTAGCTACTTCCCTCCAGCCATCAGTCATTGGGTAT
GTAAGGAATGCAAGCGTATTTCAATATTTCCCAAACCTTTAAGAAAAAAGCTTTAAGAAGGTACATCTGCAAAAGCAAA

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FIGURE 332

MGTLGQASLFAPPGNYFWSDHSAFCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWPR
ALEVDSRSVVLVSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRVYK
LTGNLTIQVAHKTGPEEDNKSRYPLIVQPCSEVLTLTNVVKLLIIDYSENRLACGSLYQG
VCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDYFPTL
SSRKLPRDPRESSAMLDYELHSDVFSSLIKIPSDTLALVSHFDIFYIYG FASGGFVYFLT VQPE
TPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKPGDSLALQ
AFNITSQDDVLFAIFSKGQKQYHHPDDSA LCAFPPIRAINLQIKERLQSCYQGEGNLELNWLL
GKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNGYSVVFVGT
KSGKLLKVRVYEFRC SNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Important features:**Signal sequence:**

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

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FIGURE 333

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAGG
CCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCCAGAGCCCACACCATGCCGGGCACCTACGC
TCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGAT
GCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCCTGGTCCTAAGGCAGGTTTACCA
GAAAGGGCTACAGGATGTTAACCTGCGCAATTTACAGCTACGGCCAGACCAGCCTGGACAGGCT
TAGAGATGGCCTCGTGGGCGCCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCG
GGATGCCCTGCGCCTCACCCTGGAGCAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTC
TGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCAT
CGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCT
GGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAA
GGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGC
AGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCG
GGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCCCGGGTGTGTGCAA
CAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGAT
GGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGA
TCACTTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGA
TGGGGCCGGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCCTGATAGAGGA
GTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAAACCTGCTGCG
GGTCTTCAGACAAGTGGAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTTGAGGACAA
GTTCCCGGATGAGCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACA
GAGTCTGACTTCAGGCCAGGAACCTCACTGAGATTCCCATACTGGACAGCCAAGTTACCAGC
CAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAGTCCTTGCAAGTTGTGGCCACCTT
CCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCCTGCCAGATGTCACTGTAGCAAGC
CACAGACACCCACAAAGTTCCCTGTGTGTCAGGCACAAATATTTCTGAAATAAATGTTTT
GGACATAG

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FIGURE 334

MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYGO
TSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALNDTQ
KLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGLTDF
GEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQLLKK
NGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLEDVSTY
PVLIEELLSRGWSEEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSSCHSDLS
RLRQRQSLTSGQELTEIPIHWTAKLPKWSVSESSPHMAPVLAVVATFPVLILWL

Important features:**N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

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FIGURE 335

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCTCAG
AGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTGCT
GCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAAAGA
CCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAAAGAA
GACTGTTTTCTCCAGATTAGAGTGGAAGAACTGGGTTCGGAGTGTCTCCTTTGTCTACTATCA
ACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCGGATCAA
AAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTGAGCAAGG
CCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTTCCATCATG
TGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGACAAAGAAGG
GAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAAATCCCAGACT
TGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAAACTGGAAGTCTGCAATTTAA
TACTGTTTCCAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTCTGTTGGATATCG
CAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGT
AGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTATGCTCAGAGGAAAGG
CTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAAAGCCACGACAATGAG
TGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGGCCGCGGCGGGCGGATC
ACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCCCATCTCTACTAAAATAC
AAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCAGCTGCTTGGGAGACAGGAGAATC
ACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGG
TAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATAAATAAATAAATAAATAAATAA
TG TAGAATTCTTACAATAAATATAGCTTGATATTC

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FIGURE 336

MARRSRHRLLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTIVSSRLEW
KKLGRSVSFVYYQQTLQGD FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTV
TLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSS
YTMNTKTGTLQFNTVSKLDTGEYSCEARNVSGYRRCPGKRMQVDDLNI SGIIAAVVVVALVIS
VCGLGVCYAQRKGYFSKETS FQKSNSSSKATTMSENVQWLTPVIPALWCAAAGGSRGQEF

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

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FIGURE 337

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCGG
CACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGCCA
TGATTTCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGAGTG
CCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGGCGG
TGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGGAGGTGTCTTCATCCC
AGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATCAGGTGT
TGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCCATGCCCT
CCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCCTACAGCTGCT
CCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCTTAGAACTCA
ATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCATGTGGGGGCAA
ACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCAGTGGGATCGGC
AGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCC
TCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCCACAATGAGGTGGGCA
CTGCCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAG
CTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCTTGTACCACCGCC
GGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCC
TGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCG
CACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTC
TCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGATGGGGCCACCCCTCAACCAA
TATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATTGATGACCCCACTCATTGGCTAAAG
GATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATGGGAAAG
AGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAAACCATCTCA
GTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATTGGGAGGAGC
CTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTACTACCAAGAGT
GAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCTTGATCTGTACCCACCCCTAT
CTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGGCTTG
GTTAGGTTTTTACTGGGGCAGAGGATAGGGAATCTCTTATTAAACTAACATGAAATATGTGTT
GTTTTCATTTGCAAATTTAAATAAAGATACATAATGTTTGTATGAAAAA

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FIGURE 439

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCTG
TCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCTGC
CCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTCCAA
GTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAGCCAAGTTGGAAGTGAAGCACTGCACC
GATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAATAGTAAAAAAT
GTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACCCTGATC
TTCATAAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 438

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCTR
RGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLASLN
TLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVP SLMRLDLGELKKLEYISE
GAFEGLFNLKYLNLGMCNIKDMPNLTPLVGLEELEMMSGNHFP EIRPGSFHGLSSLKKLWVMNS
QVSLIERNAFDGLASLVELNLAHNNLSSLP HDLFTPLRYLVELHLHNPWNCD CDILWLAWWL
REYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAELKCRTPP
MSSVKWLLPNGTVLSHASRHPRI SVLNDGTLNFSHVLLSDTG VYT CMVTNVAGNSNASAYLNV
STAE LNTSNYSFFTTVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQTTRVPKQV
AVPATD TTDKMQTS LDEV MKTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRSTVTAARTVE
IIQVDEDIPAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHW TENS LGNSLHPT
VTTISEPYIIQTHTKDKVQETQI

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FIGURE 437

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACCATGAAGCTCTTGTGGCAGG
TAACTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTTCGTCTACCTCACGGCGCAAGTGTGGATTCTGT
GTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGGCCCCAGAAGTGGCCCTCCGTTTGCTCGTGCAGTAACCAGTTCA
GCAAGGTGGTGTGCACGCGCCGGGGCCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACC
TCATGGAGAACAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTGCAGTTGG
GCAGGAAGTCCATCCGGCAGATTGAGGTGGGGGCCTTCAACGGCCTGGCCAGCCTCAACACCCTGGAGCTGTTCCG
ACAACTGGCTGACAGTCATCCCTAGCGGGGCCTTTGAATACCTGTCCAAGCTGCGGGAGCTCTGGCTTCGCAACA
ACCCCATCGAAAGCATCCCCTCTTACGCCTTCAACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCA
AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAGGGGGCTGTTCAACCTCAAGTATCTGAACTTGGGCATGTGCA
ACATTAAAGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAGGGAACCACTTCCCTG
AGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCTGAACTCACAGGTACGCCTGA
TTGAGCGGAATCTTTTGACGGGGCTGGCTTCACTTGTGGAAGTCAACTTGGCCACAATAACCTCTCTTCTTTGC
CCCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTGCATCTACACCACAACCCCTTGGAACTGTGATTGTG
ACATTCTGTGGCTAGCCTGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCCGCTGTCATGCTC
CCATGCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCCCTTCATCATGG
ACGCACCTCGAGACCTCAACATTTCTGAGGGTTCGGATGGCAGAACTTAAGTGTGGAGTCCCCCTATGTCCTCCG
TGAAGTGGTTGCTGCCCCAATGGGACAGTGCTCAGCCACGCCTCCCGCCACCCAAGGATCTCTGTCCTCAACGACG
GCACCTTGAAGTTTTCCACGTGCTGCTTTAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGCAGGCA
ACTCCAACGCCTCGGCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAAGTACAGCTTCTTACCACAG
TAACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAAGTACAAGCCTGTTCTTACCACGTCCACTG
GTTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTACAGACTACCCGTGTGCCCAAGCAGGTGGCAGTAC
CCGCGACAGACACCACTGACAAGATGCAGACCAGCCTGGATGAAGTCATGAAGACCACCAAGATCATCATTGGCT
GCTTTGTGGCAGTGAAGTCTGCTAGCTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAGCAGC
GGAGTACAGTCACAGCCCGCCGACTGTTGAGATAATCCAGGTGGACGAAGACATCCCAGCAGCAACATCCGCAG
CAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCACAATTATGACCATATTAAGT
ACAACACCTACAAACCAGCACATGGGGCCCACTGGACAGAAAACAGCCTGGGGAAGTCTCTGCACCCACAGTCA
CCACTATCTCTGAACCTTATATAATTAGACCCATACCAAGGACAAGGTACAGGAACTCAAATATGAAGTCCCCCT
CCCCCAAAAACTTATAAAATGCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTT
TTCTTGTATATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAATAATTAAGACAAAA
AGTCAAAACA

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FIGURE 436

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFH
YDCGNKTVTPVSPLGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

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FIGURE 435

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC
TGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGTCA
TCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAACTAA
ATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACTTACAG
AGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGCAGGCAA
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG
GGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATTACTTCTCAA
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCTTGGAGCCAA
GTGCAGGAGCACCACTCGCCATGTCCTCAGGCACAACCCAACTCAGGGGCCACAGCCACCACCC
TCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCATCTGAGGAGAGT
CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC
TCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT
CATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCTTTTGGCAACAATTTTA
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCTTTTTTGTGGGAAA
TCAAGTACTTCTTTGAATGATGATCTTTTCTTGCAAATGATATTGTCAGTAAATAATCACG
TTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAGAATTTTAAATTATTTAAT
AAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA
ATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 434

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCKC
SFNQKPRAPGDEEAQVENLITANATEPQKQRTQEVQPSGGSLWNLRRLLLEPLDANVDA

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FIGURE 433

[illegible]

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FIGURE 432

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCTE
AVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQQQCAQDRCNALNLTSRALDP
AGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAANVTVSLP
VRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTTVAST
TSVTTSTSAFVRPTSTTKPMPAPTSQTPRQGEHEASRDEEPRLTGGAAGHQDRSNSGQYPAK
GGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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FIGURE 431

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGCA
GGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCGTG
CAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGCGTG
GACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGCAGTG
CGGGGTTGCGGTTGCGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGCTTCTG
GCGTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTCACCTCG
CGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCCAACGGCGTGGAGTGCTACAGC
TGTGTGGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTTCGTGAGCTGCTACAAC
GCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCAGCTAATGTG
ACTGTGTCCTTGCCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGATGGAGTAACA
GGCCCAGGGTTACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAACCTCTGACCTCCGC
AACAAAGACCTACTTCTCCCCTCGAATCCCACCCCTTGTCCGGCTGCCCCCTCCAGAGCCCACG
ACTGTGGCCTCAACCACATCTGTCACCACTTCTACCTCGGCCCCAGTGAGACCCACATCCACC
ACCAAACCCATGCCAGCGCCAACCAGTCAGACTCCGAGACAGGGAGTAGAACACGAGGCCTCC
CGGGATGAGGAGCCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGACCGCAGCAATTCAGGG
CAGTATCCTGCAAAAGGGGGGCCCCAGCAGCCCCATAATAAAGGCTGTGTGGCTCCCACAGCT
GGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTCTACTGTGAGCTTCTCCACCTGGA
AATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCTCATCACTTCCTGTTCCCA
CCACTGGACTGGGCTGGCCCAGCCCCGTGTTTTTCCAACATTCCCCAGTATCCCCAGCTTCTGC
TGCGCTGGTTTGCGGCTTTGGGAAATAAAATACCGTTGTATATATTCTGCCAGGGGTGTTCTA
GCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTCTCCGCTTGTCTCTTGTGATG
TTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGGAAGGTGAGAGAGAGGATGCTAAGCTTCC
TACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGGGGTGGGTGGGACAATGGCTCCCC
ACTCTAAGCACTGCCTCCCCTACTCCCCGCATCTTTGGGGAATCGGTTCCCCATATGTCTTCC
TTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTACCCAATTCGCCCTATAGTGAGTCGTA

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FIGURE 430

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQM
LHPIFEEASDVIKEEFPNENQVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYRGQ
RSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDSNYRVFERVANILHDDC
AFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREITFEN
GEELTEEGLPFLILFHMKE DTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLHIQKTP
ADCPVIAIDSFRHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPGEQAQDV
ASSPPESSFQKLAPSEYRYTLLRDRDEL

Important features:**Signal peptide:**

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

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FIGURE 429

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGGCTCCCGGAGCCCAGCCC
TTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGACCC
CAGCGTTACCATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCT
CCTGGTAACTTGGGTTTTTACTCCTGTAACAAGTAAATAACAAGTCTTGCTACAGAGAATAT
AGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGTGCTTT
CAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATTTCCAAA
TGAAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATA
CAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATA
CAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAGTGACCCCAT
TCAAGAAATTCGGGACTTAGCAGAAATCACCCTCTTGATCGCAGCAAAAGAAATATCATTGG
ATATTTTGAGCAAAAGGACTCGGACAACCTATAGAGTTTTTGAACGAGTAGCGAATATTTTGCA
TGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAACCGGAAAGATATAGTGGCGA
CAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACTTGGGAGCTATGAC
AAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCCCTCTTGTCGGAGAAATAAC
ATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCATACTCTTTCACATGAA
AGAAGATACAGAAAGTTTAGAAATATTCAGAAATGAAGTAGCTCGGCAATTAATAAGTGAAAA
AGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACATCCTCTTCTGCACATACA
GAAAACCTCCAGCAGATTGTCTGTAATCGCTATTGACAGCTTTAGGCATATGTATGTGTTTGG
AGACTTCAAAGATGTATTAATTCCTGGAAAACCTCAAGCAATTCGTATTTGACTTACATTCTGG
AAAACCTGCACAGAGAATTCCATCATGGACCTGACCCAACCTGATACAGCCCCAGGAGAGCAAGC
CCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAACTAGCACCCAGTGAATATAG
GTATACTCTATTGAGGGATCGAGATGAGCTTTAAAAACTTGAAAAACAGTTTGTAAGCCTTTC
AACAGCAGCATCAACCTACGTGGTGAAATAGTAAACCTATATTTTCATAATTCTATGTGTAT
TTTTATTTTGAATAAACAGAAAGAAATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 428

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSAA
PGILYPGGNKYQTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRCMRHAM
CCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEGSVC
LRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLScriQKdHH
QASNSSRLHTCQRH

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

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FIGURE 427

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGCA
CGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTTGA
GTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGGTAG
CGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTCAATT
CCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTCTGCAG
TCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACAACTACC
AGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGTCCCACCC
GCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACGCTGCATGC
GTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTTCTGATCAAA
ATCATTTCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGATCATAGCACCT
TGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAAAGGACAAGAAG
GTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTAGACACTTCTGGT
CCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCATAGGAGAAAAGGCT
CTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTCTTGCCGGATACAA
AAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTCAGAGACACTTAAACCACT
ATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACCTTTTATGACCTTCATC
AACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCATTCCAATAACACCTTCCA
AAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCCTGTGATTGCAGTAAATACT
GTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGAAACTTTTAATTATTTTCT
AAAGGTGCTGCACTGCCTATTTTTCCTCTTGTTATGTAAATTTTGTACACATTGATTGTTAT
CTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATTTTCAGCTTATAGTTCTTAAAG
CATAACCCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCAAGGATCTCTTGGATGACAAAT
GATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATTTTCTGAAATGTACTATCTTAATG
CTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGAAATAAAATTTAACATTTAAAAAA
AAAAAA

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FIGURE 426

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSL LGVSKTASSREIRQAFKKLALKLH
PDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLLEDNQQGGQYESWNNYYRYDFGIYD
DDPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNCGDD
RMLCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNSIQTA
FAAGIGWLITFC SKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSANTLEDR
LAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICS NLYVFQPSLAVFK
GQGTKEYEIIHHGKKILYDILAFAKESVNSHVTTLG PQNFANDKEPWLVDFFAPWCPPCRALL
PELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSN IHEYEGHHS AEQILEFI
EDLMNPSVVS LTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMARTLTGLINVGS
IDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYS LRIWGLGFLPQVSTDLT
PQTFSEKVLQGKNHWVIDFYAPWCGPCQNFAP EFELLARMIKGKVKAGKVD CQAYAQTCQKAG
IRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLETLRNQGKR NKDEL

Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

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FIGURE 425

GAGGAACCTACCGGTACCGGCCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCACCTCCCGTGGCGCCGCGG
CTGGGCGCGTCGGAGAGTGCCTGTGCTTCTCTCCTGCACGCGGTGCTTGGGCTCGGCCAGGCGGGGTCCGCCGCCA
GGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGCGATGGCAAGGTATATTTTGTGGAATGAAAAGGA
AGTATTAGAAATGAGCTGAAGACCATTACAGATTAATATTTTGGGGACAGATTTGTGATGCTTGATTCACCCCT
TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC
TTAAATCAGAACTTGCATAAGAAAGAGAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAG
GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTACAGTTTACTTGG
AGTGTCCAAAACGCAAGCAGTAGAGAAATAAGACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAA
AAACCCGAATAACCCAAATGCACATGGCGATTTTGAAGAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA
TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA
CTATTATCGTTATGATTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGGAAAGAAGAGAATTTGATGC
TGCTGTTAATTCTGGAGAACTGTGGTTTGTAAATTTTACTCCCCAGGCTGTTACACTGCCATGATTTAGCTCC
CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTACTTCGAATTGGAGCTGTTAACTGTGGTGATGATAGAAT
GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCCAGTCTCTTCATTTTTCGGTCTGGAATGGCCCCAGTGAATA
TCATGGAGACAGATCAAAGGAGTTTAGTGAATTTTGAAGTGCAGCATGTTAGAAGTACAGTGACAGAATTTG
GACAGGAAATTTTGTCAACTCCATACAACTGCTTTTGTGCTGGTATTGGCTGGCTGATCACTTTTTTGTTCAAA
AGGAGGAGATTGTTTGAAGTACAGACACGACTCAGGCTTAGTGGCATGTTGTTTCTCAACTCATTGGATGCTAA
AGAAATATATTTGGAAGTAATACATAATCTTCCAGATTTTGAAGTACTTTCCGCAACACACTAGAGGATCGTTT
GGCTCATCATCGGTGGCTGTTATTTTTCATTTTGGAAAAATGAAAATTCAAATGATCCTGAGCTGAAAAAAT
AAAACTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGAAGTCTTCTGCACCAGACATCTGTAGTAA
TCTGTATGTTTTTCAGCCGTCTCTAGCAGTATTTAAAGGACAAGGAACCAAAGAATATGAAATTCATCATGGAA
GAAGATTCTATATGATATACTTGCCTTTGCCAAAGAAAGTGTGAATTCTCATGTTACCACGCTTGGACCTCAAAA
TTTTCTGCAATGACAAAGAACCATGGCTTGTGATTCTTTGCCCCCTGGTGTCCACCATGTCGAGCTTTACT
ACCAGAGTTACGAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTCATGA
GGGACTCTGTAACATGTATAACATTCAAGCTTATCCAACAACAGTGGTATTCAACCAGTCCAACATTCTAGTA
TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTTATGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC
ACCCACCACCTTCAACGAAGTGTACACAAAGAAAACACAACGAAAGTCTGGATGGTTGATTCTTATCTCCGTG
GTGTCATCCTTGCCAAGTCTTAATGCCAGAATGGAAGAAATGGCCCGGACATTAAGTGGACTGATCAACGTGGG
CAGTATAGATTGCCAACAGTATCATCTTTTTGTGCCAGGAAAACGTTCAAAGATACCCTGAGATAAGATTTTT
TCCCCCAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGATGCTTATTCCTGAGAAT
CTGGGCTCTAGGATTTTTACCTCAAGTATCCACAGATCAACACCTCAGACTTTCAGTGAAGAAAGTTCTACAAG
GAAAAATCATTGGGTGATTGATTTCTATGCTCTTGGTGGGACTTGGCAGAATTTTGTCCAGAATTTGCTCCAGAATTTGAGCT
CTTGGCTAGGATGATTAAAGGAAAAGTGAAGCTGGAAGAGTAGACTGTCAGGCTTATGCTCAGAGATGCCAGAA
AGCTGGGATCAGGGCCTATCCAAGTGTAAAGTTTTATTTCTACGAAAGAGCAAAGAGAAATTTTCAAGAAGAGCA
GATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAGAAATTTGGAACTCTCCGAAATCAAGGCAA
GAGGAATAAGGATGAAGTTTGAATAATGTTGAAGATGAAGAAAAAGTTTAAAGAAATTTCTGACAGATGACATCAG
AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCA
GAATTATCTACAGCACTGGTGTAAGAAAGGGTCTGCAAACTTTTCTGTAAAGGGCCGGTTTATAAATATTTTA
GACTTTCAGGCTATAATATATGGTTTACACATGAGAACAAGAATAGAGTCATCATGATTCTTTGTTATTGTGCT
TTTAACAACCTTTAAAAAATATTAACAGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTTCAGTCCATG
GACCATAGATTGCTGTCCCCCTCGACGGACTTATAATGTTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCT
ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTTCAGTTTTTTGGCTGACCTGAAAAGAGGTAAGT
TAGTTTTTGGTCACTTGTCTCTCTAAAAATGCTATCCCTAACCATATTTATATTTTCGTTTTTAAAAACACCCAT
GATGTGGCACAGTAACAAACCTGTTATGCTGTTATTATTATGAGGAGATTCTTCATTTGTTTTCTTCTCTCA
AAGGTTGAAAAATGCTTTTTAATTTTTTACAGCCGAGAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC
AAATTTGAGCAACAGTAAGTGCACAAATCTGTAGTTTGTGTATCATCCAGGAAAACCTGAGGGAAAAAATTA
TAGCAATTAAGTGGGCATTGTAGAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA
TGTGTTTCATGATTTTCTGAAATTGCTTTTATAGAAATTTTCCCACTGATAGTTGATTTTTGAGGCATCTAATAT
TTACATATTTGCTTCTGAAGTTTGTGTTTGAAGTGTATCCTTTATTTACATTGGGTTTTTCTTTTATAGTTTGG
TTTTTCACTCTGTCAGTCTATTTATTTTCAATAGGAAAAATTTTACAGTTGTTTTTCTTTTACTGTAGCTTAT
AATGATACTGTAGTTATTTCCAGTTACTAGTTTACTGTGAGAGGGCTGCCTTTTTTCAGATAAATATTGACATAA
ACTGAAGTTATTTTTATAAGAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTAGA
CTCAAAGAATCACAAATTTGTGAGTAACATGTAGTTGTTTGTAGTTATAATTCAGAGTGTACAGAATGGTAAAAAT
CCAATCAGTCAAAGAGGTCAATGAATTAAGGCTTGCACTTTTTTCAAAAAAAAAAAAAAAAAA

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FIGURE 424

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAPW
CPSCQQT DSEWEAFAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRGPG
IFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAWCSY
VFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSEERSEQNRRSEEAHRAEQLODAEEEEKDDSN
EENKDSLVDDEEEKEDLGDEDEAEEDNLAAGVDEERSEANDQGPPGEDGVTREEVEPE
EAEEGISEQPCPADTEVVEDSLRQRKSKHADKGL

Important features:**Signal peptide:**

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide
isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

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FIGURE 423

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGGC
GAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCGGC
GCCCCAACATGGCGGGGTGGGCGCTGCGGGCCCGCAGCTAACGGCGCTCCTGGCCGCCTGGATCGC
GGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCCGGGTCCA
GCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGATGCTGAAATTTTACGC
CCCATGGTGTCCATCCTGCCAGCAGACTGATTCAGAATGGGAGGCTTTTGCAAAGAATGGTGA
AATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTGGCCGCTT
CTTTGTCACCACTCTCCCAGCATTTTTTTCATGCAAAGGATGGGATATTCCGCCGTTATCGTGG
CCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATCAGTCGAGCC
TCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTCTTTTTTAGCAT
CTCTGGCAAGATATGGCATCTTCACAACTATTTACACAGTGACTCTTGGAATTCCTGCTTGGTG
TTCTTATGTGTTTTTCGTCATAGCCACCTTGGTTTTTGGCCTTTTTATGGGTCTGGTCTTGGT
GGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGCGTTCTGAGCAGAA
TCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAGGAGGAAAAAGATGA
TTCAAATGAAGAAGAAAACAAAGACAGCCTTGTAGATGATGAAGAAGAGAAAGAAGATCTTGG
CGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACTTGGCTGCTGGTGTGGATGAGGA
GAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTGACCCGGGAGGAAGTAGA
GCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCCAGCTGACACAGAGGTGGTGA
AGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGACTGTAGATTTAATGATGCGT
TTTCAAGAATACACACCAAAAACAATATGTCAGCTTCCCTTGGCCTGCAGTTTGTACCAAATC
CTTAATTTTTTCTGAATGAGCAAGCTTCTCTTAAAAGATGCTCTCTAGTCATTTGGTCTCATG
GCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGTGACAATCAGGATATAGAAAAAC
AAACGTAGTGTGGGATCTGTTTGGAGACTGGGATGGGAACAAGTTCATTTACTTAGGGGTCA
GAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCTAATCAGCACCTTCCAGAGACAAGGCTGC
AGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCTCCTGAGCATCCCCAAAGTGTAACGT
AGAAGCCTTGCATCCTTTTTCTTGTGTAAAGTATTTATTTTTGTCAAATTGCAGGAAACATCAG
GCACCACAGTGATGAAAAATCTTTCACAGCTAGAAATTGAAAGGGCCTTGGGTATAGAGAGC
AGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTGTGCTATGTTTTATTTCTTACCTTTAATT
TTTCCAGCATTTCCACCATGGGCATTACAGGCTCTCCACACTCTTCACTATTATCTCTTGGTCA
GAGGACTCCAATAACAGCCAGGTTTACATGAACTGTGTTTGTTCATTCTGACCTAAGGGGTTT
AGATAATCAGTAACCATAAACCCTGAAGCTGTGACTGCCAAACATCTCAAATGAAATGTTGTG
GCCATCAGAGACTCAAAAGGAAGTAAGGATTTTACAAGACAGATTAAAAAAAATTGTTTTGT
CCAAAATATAGTTGTTGTTGATTTTTTTTTTAAAGTTTCTAAGCAATATTTTTCAAGCCAGAAG
TCCTCTAAGTCTTGCCAGTACAAGGTAGTCTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTTC
ATCTCAAGGGGTTCCTGGGTCTTGAACACTTTAATAATAACTAAAAAACCCTTCTGATTT
TCCTTCAGTGATGTGCTTTTGGTGAAAGAATTAATGAACCTCCAGTACCTGAAAGTGAAAGATT
TGATTTTGTTCATCTTCTGTAATCTTCCAAAGAATTATATCTTTGTAAATCTCTCAATACT
CAATCTACTGTAAGTACCCAGGGAGGCTAATTTCTTT

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FIGURE 422

MDTTRYSKWGGSSSEVPGGPWGRWVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAAL
LDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAEELGEAQAKLMEQESALREL
RERVTTQGLAEAGRGREDVRTELFRALAVRLQNNNSCEPCPTSWLSFEGSCYFFSVPKTTWAAA
QDHCADASAPHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFHWNQ
GEPNDAWGRENVCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:**Type II transmembrane domain:**

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

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FIGURE 421

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCATC
GCC**ATG**GACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGCCC
TGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTCACC
ACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGCGGCG
CTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGGCGCTGGGTGCC
CTGAAGGAGGAGGTTCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTGCAGACC
ACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCTGCGGGAA
CTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACGTCCGCACT
GAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCCTGCGAGCCGTGCCCCACG
TCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGACGTGGGCGGCG
GCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCCTGGATGAGCAG
GGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGGGCTGTGCGCCAT
CTGGGCAAGGTTACAGGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTTCAGCCACTGGAAC
CAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAAGTGTGTCATGATGCTGCACACGGGGCTG
TGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAGAAAAGGCACAACCTGC
TGACCCCGCCAGTGCCCTGGAGCCGCGCCCATTCGAGCATGTCGTATCCTGGGGGCTGCTCA
CCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTTCTTCCTCATCCACCGCTGCTGAG
TCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCCTGGGCTCTGGGACCTCCA
TGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACCTCCACTAGCTCCAAAATCC
CTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAACCAAGGTTAGGTGACTGAGG
ACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGAAGCTGTTTTTGCAGCCTGAGG
AAGCATCAATAAATATTTGAGAAATGAAAAA

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FIGURE 420

MDLAGLLKSQFLCHLVFCYVFIAASGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLVM
LLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHNKFEIDFLCGWSLSERFGLLGSKVLAKKEL
AYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHRLDYPEKYFFLIHCEGTRFTEKKHEISM
QVARAKGLPRLKHLLPRTKGFAITVRSLRNVVSAVYDCTLNFRNNENPTLLGVLNGKKYHAD
LYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVNWLFWA
SLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDSKQKLND

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FIGURE 419

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAAG
GCTGCCAGGAAGGAGACGCCTTCCTGAGTCCTGGATCTTTCTTCCTTCTGGAAATCTTTGACT
GTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGCTGA
AGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATCATCA
ACACCATTCAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAAGATCA
ACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGTCGGGCA
CGGAATGCACCATCTTCACGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAATGCCATCG
TGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGAACGCTTTG
GGCTGTTAGGGGGCTCCAAGGTCCTGGCCAAGAAAGAGCTGGCCTATGTCCCAATTATCGGCT
GGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGATCGCAAGACGG
TTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTCTGATTCACTGTG
AGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCCGGGCCAAGGGGC
TGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATCACCGTGAGGAGCT
TGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTCAGAAATAATGAAAATCCAA
CACTGCTGGGAGTCCTAAACGGAAAGAAATACCATGCAGATTTGTATGTTAGGAGGATCCCAC
TGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCACAAGCTCTACCAGGAGA
AGGATGCCTTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCAGAGACGCCCATGGTGCCCC
CCCGGCGGCCCTGGACCCTCGTGAAGTGGCTGTTTTGGGCCTCGCTGGTGCTCTACCCTTTCT
TCCAGTTTCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACGCTGGCCAGCTTCATCCTCG
TCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGTGACGGAAATTGACAAGGGCT
CTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACTGACTCAGGGAGGTGTCACCAT
CCGAAGGGAACCTTGGGGAAGTGGTGGCCTCTGCATATCCTCCTTAGTGGGACACGGTGACAA
AGGCTGGGTGAGCCCCTGCTGGGCACGGCGGAAGTCACGACCTCTCCAGCCAGGGAGTCTGGT
CTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTTTTTTCCCATGTGCTTTAGTGGGC
TTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGCTGTGTGGTGAGTGTGAACTTTGTTT
TGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAGGGCAGGGCTGGGGACCGAAGGGGACA
AGTTCCCCCTTTCATCCTTTGGTGCTGAGTTTTCTGTAACCCTTGGTTGCCAGAGATAAAGTGA
AAAGTGCTTTAGGTGAGATGACTAAATTATGCCTCCAAGAAAAAAAATTAAAGTGCTTTTCT
GGGTCAAAAAAAAAAAAA

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FIGURE 418

MTKARLFRLWLVLGSVFMILLIIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRELTAD
SDVDEFLLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAERRS
VLRGFCANSSLAFTPTKERAFDDIPNSELHIVDDRHGAIYCYVPKVACTNWKRVMIIVLSGSL
LHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPFVRLI
SAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDPHTEKL
APFNEHWRQVYRLCHPCQIDYDFVGKLETLEDAQAQLLQLLQVDRQLRFPPSYRNRTASSWEE
DWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

Important features:**Signal peptide:**

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

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FIGURE 417

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGACCGGGCGCGAGGTTCCCAGCAGGA
TGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCCCAGCCCCGGGGCAG
GATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTCATGATCCTGCT
GATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGACACAGTCCTTCTCTAG
GCCGCACACGGGGCCGCGCTGCCCCAGCCCCGGGCGCGAAGAGGACAGGGAGCTCACGGCCGA
CTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGGTGGCGTGAAGCAGAGCGACCTTCC
CAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGGAGCGTGGAGGAGAGCGTGAGAGGCTACGA
CTGGTCCCCGCGCGACGCCCGGCGCAGCCCAGACCAAGGGCCGGCAGCAGGCGGAGCGGAGGAG
CGTGCTGCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCTTCCCCACCAAGGAGCGCGCATTCGA
CGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGGCCATCTACTG
CTACGTGCCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTGAGCGGAAGCCT
GCTGCACCGCGGTGCGCCCTACCGCGACCCGCTCGCATCCCGCGCGAGCACGTGCACAACGC
CAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCGGCTACGGGAAGCTCTCCCGCCACCTCAT
GAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCGACCCCTTCGTGCGCCTGAT
CTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAAAGAGGAGTTCTACCGCAAGTTCGCCGTGCC
CATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCCGCTCGGCGCGCGAGGCCTTCCGCGC
TGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGACCCGCACACGGAGAAGCT
GGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCACCCGTGCCAGATCGACTA
CGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGCAGCTGCTGCAGCTACTCCA
GGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGGACCGCCAGCAGCTGGGAGGA
GGACTGGTTCGCCAAGATCCCCTGGCCTCGAGGCAGCAGCTGTATAAACTCTACGAGGCCGA
CTTTGTTCTCTTCGGCTACCCCAAGCCCAGAAACCTCCTCCGAGACTGAAGCTTTCGCGTTG
CTTTTTCTCGCGTGCCCTGGAACCTGACGCGCAGCTCCAGTTTTTTTATGACCTACGATTT
TGCAATCTGGGCTTCTTGTTCACTCCAATGCGCTCTATCCATTGAGTACTGTATCGATATTGTT
TTTAAAGATTAATATATTTTCAGGTATTTAATACGA

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FIGURE 416

MAPQNLSTFCLLLLYLIGAVLAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFDLGAAYE
VLSDSEKRKQYDITYGEEGLKEGHQSSHGDI FSHFFGDFGFMFGGT PRQQDRNIPRGSDIIVDLEVTLEEVYAGNF
VEVVRNKPVARQAPGKRKCNCQEMRTTQLGPGRFQMTQEVVCDECPNVKLVNEERTLEVEIEPGVRDGMETPFI
GEGEPHVDGEPGDLRFRIKVVKIPIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHISRDKITRPGAKLW
KKGEGLPNFDNNNIKGLIITFVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

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FIGURE 415

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCCCCGGTGTG
AGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAGGA
GTGTGTGGAACAGGACCCGGGACAGAGGAACCAATGGGCTCCGCAGAACCTGAGCACCTTTTGCC
TGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGACGAGATTTCTATAAGATCTTGGGGG
TGCCTCGAAGTGCCCTCTATAAAGGATATTAAAAAGGCCTATAGGAACTAGCCCTGCAGCTTC
ATCCCGACCGGAACCCCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGGTGCTGCTT
ATGAGGTTCTGTCTAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAAGGATTAA
AAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCACACTTCTTTGGGGATTTTGGTTTCA
TGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATATTATTGTAG
ATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTTAGAAACAAC
CTGTGGCAAGGCAGGCTCCTGGCAAACGGAAAGTGCAATTGTCGGCAAGAGATGCGGACCACCC
AGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAATGCCCTAATGTCA
AACTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTGAGAGACGGCATGG
AGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGGAGATTTACGGTTCC
GAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATTTGTACACAAATGTGA
CAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACTCACTTGGATGGTCACA
AGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCTATGGAAGAAAGGGGAAG
GGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAATCACTTTTGATGTGGATT
TTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAACAGCTACTGAAACAAGGGT
CAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTGAATAAAATTGGACTTTGTTT
AAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTTTTGTGTGTGTTTTTGTTTT
TTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGATCATCATGAAATGAATAAGAGG
GCTTAAGAATTTGTCCATTTGCATTTCGGAAAAGAATGACCAGCAAAGGTTTACTAATACCTC
TCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCTGAGTTTCAAGAATTAAAGCTGCAAGAGG
ACTCCAGGAGCAAAGAAACACAATATAGAGGGTTGGAGTTGTTAGCAATTTCAATCAAATG
CCAACCTGGAGAAGTCTGTTTTTAAATACATTTTGTGTTATTTT

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FIGURE 414

MGPSSCLLLILILIPLLQLINPGSTQCSLDSVMDKKIKDVLNSLEYSPSPISKKLSCASVKS
QGRPSSCPAGMAVTGCACGYGCGSWDVQLETTCHCQCSVVDWTTARCCHLT

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FIGURE 413

GCCACGTTGTCTTCTTTCCTTCACCACCACCCAGGAGCTCAGAGATCTAAGCTGCTTTCCATC
TTTTCTCCCAGCCCCAGGACACTGACTCTGTACAGGATGGGGGCCGTCCTCTTGCCTCCTTCTC
ATCCTAATCCCCCTTCTCCAGCTGATCAACCCGGGGAGTACTCAGTGTTCCCTTAGACTCCGTT
ATGGATAAGAAGATCAAGGATGTTCTCAACAGTCTAGAGTACAGTCCCTCTCCTATAAGCAAG
AAGCTCTCGTGTGCTAGTGTCAAAAGCCAAGGCAGACCGTCCTCCTGCCCTGCTGGGATGGCT
GTCAGTGGCTGTGCTTGTGGCTATGGCTGTGGTTCGTGGGATGTTACAGCTGGAAACCACTGC
CACTGCCAGTGCAGTGTGGTGGACTGGACCACTGCCCCGCTGCTGCCACCTGACCTGACAGGGA
GGAGGCTGAGAACTCAGTTTTGTGACCATGACAGTAATGAAACCAGGGTCCCAACCAAGAAAT
CTAACTCAAACGTCCCACTTCATTTGTTCCATTCTGATTCTTGGGTAATAAAGACAACTTT
GTACCTCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 412

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNID
YPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPREGFWCLNREQRP
GQNC SNYTVRFLCPPGSLRRDTERIWS PWS PWSKCSAACGQTGVQTRTRICLAEMVSLCSEAS
EEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTKTPKL
LTQTDSDGRFRIPLGCPDGKSILKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPYMVMNP
ETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRLKQQHQAGEYFCKA
QSDAGAVKSKVAQLIVTASDET PCNPVPESYLIRLPHDCFQ NATNSFYVDVGRCPVKTCAGQQ
DNGIRCRDAVQNC CGISKTEEREIQCSGYTLPTKVAKECSCQRCTETRSIVRGRVSAADNGEP
MRFGHVYMGNSRVSM TGYKGTFTLHVPQDTERLVLT FVDRLQKFVNTTKVLFPNKKGS AVFHE
IKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSR SFYRQNGEPYIGKVKASVTFLDPR
NISTATAAQTDLNF INDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHLDSTQVKMPEHI
STVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLENLDVPESRRCFVKV
RAYRSE RFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGACVPAFCDDQSPDA
YSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLN YRRTDHEDPRVKKTA FQISMAKPR
PNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTPFNEDDPM SWTEDYLAWW
PKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRSTRDRDQPNVSAACLEF
KCSGMLYDQDRVDRTL VKVIPQGSRRASVNPMLHEYLVNHLPLAVNNDTSEYTMLAPLDPLG
HNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALTENCVERQVGRQSAFQYLQ
STPAQSPAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVAQQPLIN

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FIGURE 411

CCCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAACTTCCCAGGGGACCGCATTCCAGAGTCA
GTGACTCTGTGAAGCACCCACATCTACCTCTTGCCACGTTCCCACGGGCTTGGGGGAAAAGATGGTGGGGACCAAG
GCCTGGGTGTTCTCCTTCCTGGTCTGGAAGTCACATCTGTGTGGGGAGACAGACGATGCTCACCAGTCAGTA
AGAAGAGTCCAGCCTGGGAAGAAGAACCCAGCATCTTTGCCAAGCCTGCCGACACCCTGGAGAGCCCTGGTGAG
TGGACAACATGGTTCAACATCGACTACCCAGGCGGGAAGGGCGACTATGAGCGGCTGGAGCCATTCTGCTTCTAC
TATGGGGACCGTGTATGTGCCCCCTCCCTGCGGCTAGAGGCTCGGACCCTGACTGGACACCTGCGGGCAGCACT
GGCCAGGTGGTCCATGGTAGTCCCCGTGAGGGTTTCTGGTGCCTCAACAGGGAGCAGCGGCTGGCCAGAACTGC
TCTAATTACACCGTACGCTTCTCTGCCACAGGATCCCTGCGCCGAGACACAGAGCGCATCTGGAGCCCATGG
TCTCCCTGGAGCAAGTGTCTAGCTGCCTGTGGTCAGACTGGGGTCCAGACTCGCACACGCATTTGCTTGGCAGAG
ATGGTGTGCTGTGTCAGTGAGGCCAGCGAAGAGGGTCAGCACTGCATGGGCCAGGACTGTACAGCCTGTGACCTG
ACCTGCCCAATGGGCCAGGTGAATGCTGACTGTGATGCCTGCATGTGCCAGGACTTCATGCTTTCATGGGGCTGTC
TCCCTTCCCGGAGGTGCCCCAGCCTCAGGGGCTGCTATCTACCTCCTGACCAAGACGCCGAAGCTGCTGACCCAG
ACAGACAGTGATGGGAGATTCCGAATCCCTGGCTTGTGCCCTGATGGCAAAAGCATCCTGAAGATCACAAAGGTC
AAGTTTGGCCCCATTGTACTCACAAATGCCAAGACTAGCCTGAAGGCAGCCACCATCAAGGCAGACTTTGTGAGG
GCAGAGACTCCATACATGGTGTGAACCTGAGACAAAAGCACGGAGAGCTGGGCAGAGCGTGTCTGTGTGCTGT
AAGCCACAGGGAAGCCAGGCCAGACAAGTATTTTGGTATCATAATGACACATTGCTGGATCCTTCCCTCTAC
AAGCATGAGAGCAAGCTGGTGTGAGGAACTGCAGCAGCACCAGGCTGGGGAGTACTTTTGAAGGCCAGAGT
GATGCTGGGGCTGTGAAGTCCAAGGTTGCCAGCTGATTGTACAGCATCTGATGAGACTCCTTGAACCCAGTT
CCTGAGAGCTGTGTCAGTGAGGCTGCCCATGATTGCTTTGAGAATGCCACCAACTCCTTCTACTATGACGTGGGA
CGCTGCCCTGTAAAGACTTGTGACAGGGCAGCAGGATAGGATGAGGTGCCGTGATGCTGTCAGAACTGCTGT
GGCATCTCCAAGACAGAGGAAAGGGAGATCCAGTGCAGTGGCTACACGCTACCCACCAAGGTGGCCAAGGAGTGC
AGCTGCCAGCGGTGACGGAAGCTCGGAGCATCGTGGGGGCGGTGTGAGTGTGCTGACAATGGGGAGCCCATG
CGCTTTGGCCATGTGTACATGGGGAAACAGCCGTGTAGCATGAGTGGCTACAAGGGCACTTTACACCTCCATGTC
CCCCAGGACACTGAGAGGCTGGTGTACATTTGTGGACAGGCTGCAGAACTTTGTCAACACCACCAAGTGTCTA
CCTTTCAACAAGAAGGGGAGTGCCGTGTTCCATGAATCAAGATGCTTCGTCCGAAAGAGCCCATCACTTTGGAA
GCCATGGAGACCAACATCATCCCCCTGGGGGAAGTGGTTGGTGAAGACCCCATGGCTGAAGCTGGAGATTCATCC
AGGAGTTTCTACAGGCAGAATGGGGAGCCCTACATAGGAAAAGTGAAGGCCAGTGTGACCTTCTGGATCCCCGG
AATATTTCCACAGCCACAGCTGCCAGACTGACCTGAACCTTCAATGACGAAGGAGACACTTTCCCCCTTCGG
ACGTATGGCATGTTCTCTGTGGACTTCAGAGATGAGGTACCTCAGAGCCACTTAATGCTGGCAAGTGAAGTGC
GACCTTGACTCGACCCAGGTCAAGATGCCAGAGCATATCCACAGTGAAACTCTGGTCACTCAATCCAGACACA
GGCTGTGGGAGGAGGAAGGTGATTTCAAATTTGAAAATCAAGAGGAGGAACAAAGAGAGACAGAACTTCCTG
GTGGGCAACCTGGAGATTCTGTGAGAGGAGGCTCTTTAACCTGGATGTTCTCTGAAAGCAGGGGCTGTTGTAAG
GTGAGGGCTTACCGGAGTGAGAGGTTCTTGCTAGTGAGCAGATCCAGGGGGTGTGATCTCCGTGATTAACCTG
GAGCCTAGAAGTGGCTTCTTGTCCAACCTTAGGGCTGGGCGCTTTGACAGTGTGTCACAGGCCCCAACGGG
GCCTGTGTGCTGCTTCTGTGATGACCACTGCCCTGATGCCTACTCTGCTATGCTTGGCAAGCCTGGCTGGG
GAGGAAGTGAAGCAGTGGAGTCTTCTCTAAATTCACCCAAATGCAATTGGCGTCCCTCAGCCCTATCTCAAC
AAGTCAACTACCGTCCGACGGACCATGAGGATCCACGGGTTAAAAAGACAGTTTCCAGATTAGCATGGCCAAG
CCAAGGCCCAACTCAGCTGAGGAGAGCAATGGGCCCATCTATGCCTTTGAGAACCCTCCGGGCATGTGAAGAGGCA
CCACCCAGTGCAGCCCACTTCCGGTCTACAGATTGAGGGGGATCGATATGACTACAACACAGTCCCCCTCAAC
GAAGATGACCCATGAGCTGGACTGAAGACTATCTGGCATGGTGGCCAAAGCCGATGGAATTCAGGGCCTGTCTAT
ATCAAGGTGAAGATTGTGGGGCCACTGGAAGTGAATGTGCGATCCCGCAACATGGGGGGCACTCATCGGCGGACA
GTGGGGAAGCTGTATGGAATCCGAGATGTGAGGAGCACTCGGGACAGGGACAGCCCAATGTCTCAGCTGCCTGT
CTGGAGTTCAAGTGCAGTGGGATGCTCTATGATCAGGACCGTGTGGACCGCACCTTGGTGAAGGTCACTCCCCAG
GGCAGCTGCCGTGAGCCAGTGTGAACCCCATGCTGCATGAGTACCTGGTCAACCACTTGGCACTTGCAGTCAAC
AACGACACCAGTGAGTACCCATGCTGGCACCTTGGACCCACTGGGCCACAACATATGGCATCTACACTGTCACT
GACCAGGACCTCGCACGGCCAAGGAGATCGCGCTCGGCCGCTGCTTTGATGGCACATCCGATGGCTCCTCCAGA
ATCATGAAGAGCAATGTGGGAGTAGCCCTCACCTTCAACTGTGTAGAGAGGCAAGTAGGCCGCCAGAGTGCCTTC
CAGTACCTCCAAAGCACCCAGCCAGTCCCTGCTGCAGGCACTGTCCAAGGAAGAGTGGCCTCGAGGAGGAGCAG
CAGCGAGCGAGCAGGGGTGGCCAGCGCCAGGGTGGAGTGGTGGCCTCTCTGAGATTCTCTAGAGTTGCTCAACAG
CCCCTGATCAACTAAGTTTTGTGGTACTTCACCCTCTTCTGCCCTCATTTTCATGTGACAGCCATTGTGAGACTGA
TGCACAACTGTCACTTGGTTAATTTAAGCACTTCTGTTTTCGTGAATTTGCTTGTGTTTCTTCTATGCCTTTA
CTTACTTTGTCCCATGCTACTGATTGGCACGTGGCCCCCAATGGCACAATAAAGCCCTTTGTGAAGTCACTGTTT
TTTAAATGAAACACAAGAAATTGGCCACTGGTAAAACCTCTGCAGCTTCAACTGTACTTCATTTAATGCCATTAAT
GCAATATACTTCTCTCTTTTTGTGATGGTTTTGCCACCTCTGCAATAGTGATAATCTGATGCTGAAGATCAA
ATAACCAATATAAAGCATATTTCTTGGCCTTGTCTCCACAGGACATAGGCAAGCCTTGATCATAGTTTCATACAT
AAATGGTGGTGAATAAAGAAATAAACAACAATACTTTTACTTGAAATGTAAATAACTTATTTATTTCTTTGCTA
AATTTGGAATTTCTAGTGACATTCAAAGTTAAGCTATTAATATAGGGTGATCATAGTTCCCTCTACCAAGTCTGG
AAAGAACATCTCCTGGTATCCACAATTACACCAAGGTTGTCTAAGTATTTGTACATTTCCCTTTCATTGCTTT
TGTTCTTGTAGAAACCCAGTGTAGCCAGGGCAGATGTCAATAAATGCATACTCTGTATTTGAAAAA

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FIGURE 410

MGDKIWLPPFVLLLAALPPVLLPGAAGFTPSLDSDFTFLLPAGQKECFYQPMPLKASLEIEYQ
VLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMECFDNTFSTISEKVIFFELIL
DNMGEQAQEEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRNIQE
SNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

Important features:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

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FIGURE 409

CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC
CTCTTTTCAGCCCGGGATCGCCCCAGCAGGGATGGGCGACAAGATCTGGCTGCCCTTCCCCGTGCTCCTTCTGGCC
GCTCTGCCTCCGGTGCTGCTGCCTGGGGCGGGCGGCTTCACACCTTCCCTCGATAGCGACTTCACCTTTACCCTT
CCCGCCGGCCAGAAGGAGTGCTTCTACCAGCCCATGCCCTGAAGGCCCTCGCTGGAGATCGAGTACCAAGTTTTA
GATGGAGCAGGATTAGATATTGATTTCCATCTTGCCTCTCCAGAAGGCCAAAACCTTAGTTTTTGAACAAAGAAAA
TCAGATGGAGTTCACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTTCAGCACCATT
TCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAAGAAGATTGGAAG
AAATATATTACTGGCACAGATATATTGGATATGAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCC
AGACTAAGCAAAAGTGGGCACATACAAATTCGCTTAGAGCATTTGAAGCTCGTGATCGAAACATACAAGAAAGC
AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTCATGGTGGTGGTGTGAGCCATTCAAGTTTAT
ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTTAAACTCCAACTAGAGTACGTAACATTGAAA
AATGAGGCATAAAAATGCAATAAACTGTTACAGTCAAGACCATTAAATGGTCTTCTCCAAAATATTTTGAGATATA
AAAGTAGGAAACAGGTATAATTTTAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAG
TTGTAATTAAGTGTGTAACAGGAATATTTTGCAGAATATAGGTTAACTGAATGAAGCCATATTAATAACTGCAT
TTTCCTAACTTTGAAAAATTTTGCAAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCTAATTGCAACACC
AGTCTGTTTTTAAACAGGTTCTATTACCCAGAACTTTTTTGTAAATGCGGCAGTTACAAATTAACGTGTGGAAGTTT
TCAGTTTTAAGTTATAAATCACCTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCCCAA
CTTTTCTCTATTTACATATGCATCTCTCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTG
AGATTTTTTATAACCAAATACATTTTCAGTGTAAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC
CCAAAAGCTGACATTTTCACGATTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACATGTTTTCTCTTTG
AAATGAAGAATATAGTTTTAAAGCTTCTCTCCATAGGGACACATTTTCTCTAACCGTTAACTAAAGTGTAGGA
TTTTAAATTAATGTGAGGTAAAATAAGTTTTATTTTTAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA
TAATCATGTTATGTTAATTTTAAACATGATTGCTGACTTGGATAATTCATTATTACCAGCAGTTATGAAGGAAATA
TTGCTAAAATGATCTGGGCCTACCATAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAACAGGAA
AGAATTTAGAAAACTTGAGAAAACCTAATCCAAAATAAAATTCACTTAAGTAGAACTATAAATAAATATCTAGA
ATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG
AACTTTGGCTGTAGGTTTTTATTTTCTACAAGAATTCTGGTTTGAATTATTTTGTGAAGCAGGTACATTTTATA
AAATGTAAGCCCTACTGTAAGGTTTAGCACTGGGTGTACATATTTATTAATAATTTTATTATATACAACTTTTTAT
TAAATGGCCTTTCTGAACACTTTATTTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTTTTTAAA
CACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTTGAAGTCTATGGGGGTCTTAC
TCAAGTACTAGTAATTTAACTTCATCATGAATGAATATAATTTTTAAGTTATGCCCATTTATAACGTTGTTTTAT
GACTACATTGTGAGTTAGAAACAACTTAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATT
CTTGATGAGCAATAATGATAACCAGAGAGTGATTTCAATTTACACTCATAGTAGTATAAAAAGAGATACATTTCCC
TCTTAGGCCCTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAAATGCCGTAT
ATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAGAACAA
AGGTCAATAAGATCCTTGCCATATGAATACCCCTCCCTTTTGCCTGTTAAATTTGCAATGAGAAGCAAATTTACA
GTACCATAACTAATAAAGCAGGGTACAGATATAAATACTGTCATCTTTTCTATAAACTGTGATTAAGAAATCTA
CCTCTCCTGTATGGCTGTTACTGTACTGTACTCTGACTCCTTACCTAACAAATGAATTTGTTACATAATCTTCT
ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTTCAGTAACCTTCTTACCATATAAAAACGATAATTGCTT
TATTTGGAAAAGAATTTAGGAATACTAAGGACAATTTATTTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG
CATAACCAAAAAAGCAAACTTGTAACAGAGTAAAAATCTTTAATATTTCTAAAGACATACTGTTTATCTGCTT
CATATGCTTTTTTTAATTTCACTATTCCATTTCTAAATTAAGTTATGCTAAATTGAGTAAGCTGTTTATCACTT
AACAGCTCATTTTGTCTTTTTCAATATACAAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATTTT
CATAATGTAGCAGTTACCGTGTTTACCTCACACTAAGGCCTAGAGTTTGCTCTGATATGCATTTGGATGATTAAT
GTTATGCTGTTCTTTTCATGTGAATGTCAAGACATGGAGGTGTTTGAATTTTATGGTAAATTAATCCTTCTTA
CACATAATGGTGTCTTAAATTTGACAAAAAATGAGCACTTACAATTGTATGTCTCCTCAAATGAAGATTCTTTAT
GTGAAATTTTAAAGACATTGATTCCGCATGTAAGGATTTTTTTCATCTGAAGTACAATAATGCACAATCAGTGTTG
CTCAAACCTGCTTTTATACTTATAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATA
AAATTATCAAAGGAAAA

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FIGURE 408

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALDY
EADGSTNNGIFQINSRRWCSNLTPNVPNVCRMYSDDLNPNLKDTVICAMKITQEPQGLGYWE
AWRHHCQGKDLTEWVDGCDF

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

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FIGURE 407

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGAG
CCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTCGC
TCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCTGGA
CTTGAGAAATCCTCCGCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAAGCCC
TGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAAAGCTC
AGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAGCAGGGC
TCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGCTCAGCTG
CCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTGCTACATGA
CTTCGGGCTGGAGGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGCTTATTTAC
AAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACAACGGGATCTT
CCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAACGTGTGCCGGAT
GTA CTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGCCATGAAGATAAC
CCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCTGGAGGCATCACTGCCAGGGAAAAGACCT
CACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCACAGCAGGCTGGGAA
ATGTGGTTTGTTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATAAAGGATGGTTGAACG
TGAAA

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FIGURE 406

MTPQSLLQTTFLLSLLFLVQGAHGRGHREDFRCSQRNQT RSSLHYKPTPDLRISIENSEE
ALT VHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLY GKRDFLLSDKASSLLCFQHQE
ESLAQGPPLLATSVTSWWSPQNI SLPSAASFTFSFHSPHTA HNASVDMCELKRDQLLSQF
LKHPQKASRRPSAAPASQQQLQSLESKLT SVRFMGDMVSFEED INATVWKLQPTAGLQDLHIH
SRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVD FSS DALFQDKNSSQVLGEKVLGI
VVQNTKVANLTEPVVLT FQHQLQPKNVT LQCVFWVEDPTLSSP HWSAGCETVRRETQTSCF
CNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVV SALACLVTIAAYLCSRVP LPCRKRPRDY
TIKVH MNLLLAVFLDTSFLLSEPVALTGSEAGCRASAI FLHFSI LTCLSWMGLEGYNLYRLV
VEVFGTYVPGYLLKLSAMGWGFPI FLVTLVALVDVDNYGPIILAV HRTPEGVIYPSMCWIRDS
LVSYITNLGLFSLVFLFNMA MLATMVVQILRLRPHTQKWSHVLT LGLSLVLGLPWALIFFSF
ASGTFQLVVLYLFSIITSFQGF LIFIWYWSMRLQARGGPSPLKSN SARLPISSGSTSSSRI

Important features:**Signal peptide:**

amino acids 1-25

Putative transmembrane domains:amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657**Microbodies C-terminal targeting signal.**

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344**G-protein coupled receptors family 2 proteins**

amino acids 475-504

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FIGURE 405

GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCCAGACCTGGAGGGTCTCGCTCTGTCA
CACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACCTCCCGGGTTCAAGTGATTCTCATGCC
TCAGCCTCCCGAGTAGCTGGGATTACAGGTGGTGACTTCCAAGAGTGACTCCGTCCGAGGAAAATGACTCCCCAG
TCGCTGCTGCAGACGACACTGTTCTGCTGAGTCTGCTCTTCTGGTCCAAGGTGCCACGGCAGGGGCCACAGG
GAAGACTTTCGCTTCTGCAGCCAGCGGAACCAGACACACAGGAGCAGCCTCCACTACAAACCCACACCAGACCTG
CGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCTTTCCCTGCAGCCCACCTGCTTCCCGA
TCCTTCCCTGACCCAGGGGCTCTACCACTTCTGCCTCTACTGGAACCGACATGCTGGGAGATTACATCTTCTC
TATGGCAAGCGTGACTTCTTGCTGAGTGACAAAGCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAGCCTG
GCTCAGGGCCCCCGCTGTTAGCCACTTCTGTCACTCCTCTGGTGGAGCCCTCAGAACATCAGCCTGCCAGTGCC
GCCAGCTTACCTTCTCCTTCCACAGTCTCTCCACACGGCCGCTCACAATGCCTCGGTGGACATGTGCGAGCTC
AAAAGGGACCTCCAGCTGCTCAGCCAGTTCTGAAGCATCCCCAGAAGGCCTCAAGGAGGCCCTCGGCTGCCCC
GCCAGCCAGCAGTTGCAGAGCCTGGAGTCGAAACTGACCTCTGTGAGATTTCATGGGGGACATGGTGTCTTCGAG
GAGGACCGGATCAACGCCACGGTGTGGAAGCTCCAGCCACAGCCGGCCTCCAGGACCTGCACATCCACTCCCGG
CAGGAGGAGGAGCAGAGCGAGATCATGGAGTACTCGGTGCTGCTGCCTCGAACACTCTTCCAGAGGACGAAAGGC
CGGAGCGGGGAGGCTGAGAAGAGACTCCTCCTGGTGGACTTCAGCAGCCAAAGCCCTGTTCCAGGACAAGAATTCC
AGCCAAGTCTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAAGTAGCCAACTCAGGAGCCCTG
GTGCTCACTTTCAGCACCAGCTACAGCCGAAGAATGTGACTCTGCAATGTGTGTTCTGGGTTGAAGACCCACA
TTGAGCAGCCCCGGGCGATTGGAGCAGTGTGGGTGTGAGACCGTCAGGAGAGAAACCCAAACATCCTGCTTCTGC
AACCCTTGACCTACTTTCAGTGCTGATGGTCTCCTCGGTGGAGGTGGACGCCGTGCACAAGCACTACCTGAGC
CTCCTCTCCTACGTGGGCTGTGCTGCTCTGCCCTGGCCTGCCTGTCACTTGCCTGCTGCTGGCCGTCTTC
GTGCCCCCTGCCGTGCAGGAGGAAACCTCGGGACTACACCATCAAGGTGCACATGAACCTCAGGAGCCAGTGC
CTGCTGGACACGAGCTTCTGCTCAGCGAGCCGGTGGCCCTGACAGGCTCTGAGGCTGGCTGCGGAGCCAGTGC
ATCTTCTGCACTTCTCCTGCTCACCTGCCTTTCTGGATGGGCCCTCGAGGGGTACAACCTCTACCGACTCGTG
GTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTT
CTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAATATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAG
GGCGTCATCTACCTTCCATGTGCTGGATCCGGGACTCCCTGGTCACTACATACCAACCTGGGCTTCTTCAGC
CTGGTGTCTTCTGTTCAACATGGCCATGCTAGCCACCATGGTGGTGCAGATCCTGCGGCTGCGGCCAGCCAA
AAGTGGTCACATGTGCTGACACTGCTGGGCCTCAGCCTGGTCTTGGCCTGCCCTGGGCCTTGATCTTCTCTCC
TTTGCTTCTGGCACCTTCCAGCTTGTGCTCCTCTACCTTTTTCAGCATCATCACCTCCTTCCAAGGCTTCTCATC
TTCATCTGGTACTGGTCCATGCGGCTGCAGGCCCGGGGTGGCCCCCTCCCTCTGAAGAGCAACTCAGACAGCGCC
AGGCTCCCCATCAGCTCGGGCAGCACCTCGTCCAGCCGCATCTAGGCTCCAGCCACCTGCCCATGTGATGAAG
CAGAGATGCGGCCCTCGTCGACACTGCTGCGCCCCGAGCCAGGCCAGCCCCAGGCCAGTCCAGCCGAGACT
TTGGAAGGCCAACGACCATGGAGAGATGGGCGTGGGACTGGGACGGACTCCCGGGCTGGGCTTTGAATTG
GCCTTGGGGACTACTCGGCTCTCACTCAGCTCCCACGGGACTCAGAAGTGCGCCGCCATGCTGCCTAGGGTACTG
TCCCCACATCTGTCCCAACCCAGCTGGAGGCCTGGTCTCTCCTTACAACCCCTGGGCCAGCCCTCATTGCTGGG
GGCCAGGCCTTGGATCTTGAGGGTCTGGCACATCCTTAATCCTGTGCCCTGCCTGGGACAGAAATGTGGCTCCA
GTTGCTCTGTCTCTCGTGGTCAACCTGAGGGCACTCTGCATCCTCTGTCAATTTAACCTCAGGTGGCACCCAGGG
CGAATGGGGCCAGGGCAGACCTTCAGGGCCAGAGCCCTGGCGGAGGAGAGGCCCTTGGCAGGAGCACAGCAGC
AGCTCGCCTACCTCTGAGCCCAGGCCCTCCCTCCCTCAGCCCCCAGTCCCTCCCTCATCTTCCCTGGGGTTC
TCCTCCTCTCCAGGGCCTCCTTGTCTCCTCGTTCACAGCTGGGGGTCCCCGATTCCAATGCTGTTTTTTGGGGA
GTGGTTTTCCAGGAGCTGCCTGGTGTCTGCTGTAAATGTTTGTCTACTGCACAAGCCTCGGCCTGCCCTGAGCCA
GGCTCGGTACCGATGCGTGGGCTGGGCTAGGTCCCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATTGCCCTTG
CTACCTGACCAAGCACACGCCTCAGAGGGGCCCTCAGCCTCTCCTGAAGCCCTCTTGTGGCAAGAAGTGTGGA
CCATGCCAGTCCCGTCTGGTTTCCATCCCACCCTTCAAGGACTGAGACTGACCTCCTCTGGTGACACTGGCCTA
GAGCCTGACACTCTCCTAAGAGGTTCTCTCAAGCCCCCAATAGCTCCAGGCGCCCTCGGCGGCCCATCATGGT
TAATTCTGTCCAACAAACACACAGGGTAGATTGCTGGCCTGTTGTAGGTGGTAGGGACACAGATGACCGACCTG
GTCACCTCCTGCCAACATTCACTGCTGGTATGTGAGGCGTGCCTGAAGCAAGAAGTCTGGAGCTACAGGGACA
GGGAGCCATCATTCTGCTGGGAATCCTGGAAGACTTCTGAGGAGTCAAGCTTCAATCTTGACCTTGAAGAT
GGGAAGGATGTTCTTTTACGTACCAATTCTTTGTCTTTTGTATTTAAAGAAAGTACATGTTTATTGTAGAGA
ATTTGGAAGATGTAGAAGAGAATCAAGAAGAAAAATAAAATCAGCTGTTGTAATCGCCTAGCAAAAAAAAAA
AAA

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FIGURE 404

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFRD
EVEDDYFRTWSPGKPFQALDPAKDPCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEAGV
DHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCPGPSDK
PTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTKTLLRPERSRFDTSILPICKDS
LGWMFNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNEWCYCFQRQQDP
PCQTELSNIQKRQGVKKLLGQYIPLCDEDGYKPTQCHGSVGQCWCVDTRYGNEVMGSRINGVA
DCAIDFEISGDFASGDFHEWTDDEDDDDIMNDEDEIEDDDDEDEGDDDDGGDDHDVYI

Important features:**Signal peptide:**

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

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FIGURE 403

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGAAAGCAGCGAGTTG
GCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCTCACAACAAGATGCTCAAGGTGTCAGC
CGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCAGTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGG
GCGGTTCGGACGGCGGTAATTTTCTGGATGATAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGG
ACAGTGGAACAAATTCCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCCCTTCGATCA
GGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTATGCATTGCTCAAGATTC
TCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATGAAAGAAGCAGGAGTAGACCATAGGCAGTG
GAGGGGTCCCATATTATCCACCTGCAAGCAGTGCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCA
TACCTACTCTTTTCAGTGCAAAC TAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGG
ACATTGCCCATGTCCTTCAGATAAGCCCACCACTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCTGGAGTT
CAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAAGTCAAAACAAGAAGACAAA
AACATTGCTGAGGCCCTGAGAGAAGCAGATTGATACACAGCATCTTGCCAATTTGCAAGGACTCACTTGGCTGGAT
GTTTAACAGACTTGATACAACTATGACCTGCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAA
TGAACAGTGATACCAAGGCATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTG
CTACTGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCAAGGGGTAAA
GAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGCCAACACAATGTCATGGCAGTGT
TGGAACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTCATGGGATCCAGAATAAATGGTGTGTCAGATTGTGC
TATAGATTTTGGAGATCTCCGGAGATTTTGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGA
CGATATTATGAATGATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGAAGA
CCATGATGTATACATTGATTGATGACAGTTGAAATCAATAAATTTCTACATTTCTAATATTTACAAAAATGATAG
CCTATTTAAATATCTTCTTCCCAATAACAAAATGATTCTAAACCTCACATATATTTGTATAATTATTTGAA
AAATTGCAGCTAAAGTTATAGAATTTATGTTTAAATAAGAATCATTTGCTTTGAGTTTTTATATTCCTTACACA
AAAAGAAAATACATATGCAGTCTAGTCAGACAAAATAAAGTTTGAAGTGCTACTATAATAAATTTTTCACGAGA
ACAACTTTGTAAATCTTCATAAGCAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAGAT
AATTCTAAGTGAAATTTAAATAAATAAATTTTAAATGACCTGGGTCTTAAGGATTTAGGAAAAATATGCATGCT
TTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAGGATAACAGAGAGATACCACATGACTCCA
AAAAAAAAAAAAA

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FIGURE 402

MACRCLSFLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAGS
APRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVPEDDADYYCSVGYGFS

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FIGURE 401

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCTG
CCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCTGT
CAGTTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGGCTC
AACTCTCCTGCACGCTCAGCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCTGGTACC
AGCAGCGGGCAGGCAGTGCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCACCACC
GGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCACAATGCCTGTGTCC
TCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGCTACGGCT
TTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTTCTGCCCTGA
CCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAAATGGGTTAATAATA
TTCAACATGTCAACAAC

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FIGURE 400

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRTSKDPEHEG
CYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVVDWLPL
AHQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTVGRI
TGLDPAGPMFEGADIIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDFQPGC
GLNDVLGSIAYGTITEVVKCEHERAVHLFVDSL VNQDKPSFAFQCTDSNRFKKGICLSCRKNR
CNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

Important features:**Signal peptide:**

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

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FIGURE 399

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGGC
TCCGTGCCGCCAAGTTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCCAGCCCCTGGCCGAG
AGAAGGGTCTTACCGGCCGGGATTGCTGGAAACACCAAGAGGTGGTTTTTGTTTTTTAAACT
TCTGTTTCTTGGGAGGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCCCTCTGCTCTGTTTC
TGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGACGGCTG
GAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGGTTTAAC
CTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTCCGCCACAGCCAGCCC
TTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTTCATCATTACGGATGGACGATG
AGCGGTATCTTTGAAAACCTGGCTGCACAACTCGTGTGAGCCCTGCACACAAGAGAGAAAGAC
GCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCACCAGCTTTACACGGATGCGGTCAAT
AATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGGAGAAGGACGAT
TTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTGGCCGGGTATGCA
GGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGCCGGGGCCCATGTTT
GAAGGGGGCCGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTGTGGATGTCCTCCAC
ACCTACACGCGTTCCTTCGGCTTGAGCATTGGTATTCAGATGCCTGTGGGCCACATTGACATC
TACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGTCTTGGGATCAATTGCA
TATGGAACAATCACAGAGGTGGTAAAATGTGAGCATGAGCGAGCCGTCCACCTCTTTGTTGAC
TCTCTGGTGAATCAGGACAAGCCGAGTTTTTGCTTCCAGTGCAGTACTCCAATCGCTTCAAA
AAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCATTGGCTACAATGCCAAGAAA
ATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGGCAGGCATGCCTTTCAGAGGT
AACCTTCAGTCCCTGGAGTGTCCCTTGAGGAAGGCCCTTAATACCTCCTTCTTAATACCATGCT
GCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCACAAATCCAATCAAATCGTTGCAA
ATCAGATTACACTGTGCATGTCCTAGGAAAGGGAATCTTTACAAAATAAACAGTGTGGACCCC
TAATAA

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FIGURE 398

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyGETGRL
FTESCSISPKLRSIAVYYDNPHMVPPDKCRCAVGSILSEGEESPSPELIDLYQKFGFKVFSFP
APSHVVTATFPYTTILSIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCPARQGD
FYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAA TLSPGASSRGW
DDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEKGKE

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FIGURE 397

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCCATGTCGGACCTGCTAC
TACTGGGCCTGATTGGGGGCCTGACTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGGGT
ACTCAGGGCTACTGGCTGGGGTGGAAAGTGAGTGCTGGGTCACCCCCCATCCGCAACGTCACTG
TGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGCTGCA
GCATCTCTCCCAAGETCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCCCCCTG
ATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCCCTGAGC
TCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGCCATGTGG
TGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCGTGTCCATC
CTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGGAGATCTACC
AGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTATGTGCCTGAGA
TGAAGGAGACAGAGTGGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCCAGGTGGATGGCA
CAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAAGTGAGCCCTGGCAGCCGGG
AGACTTCAGCTGCCACACTGTCACCTGGGGCGAGCAGCCGTGGCTGGGATGACGGTGACACCC
GCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGAGGAGCTGGACTTGG
AGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGCCCCTGGGGACTACCA
AGTGGCTCTGGGAGCCCACTGCCCCTGAGAAGGGCAAGGAGTAACCCATGGCCTGCACCCTCC
TGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCTCCAGCCCTCTTCCTCCT
TCCTCTGGGGGAGGAGGGGTTCCTGAGGGACCTGACTTCCCCTGCTCCAGGCCTCTTGCTAAG
CCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCAGGGACTATTTTCTGCACCA
GCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTTCAGACTCACAGTGGAGCTTCCAGGACC
CAGAATAAAGCCAATGATTTACTTGTTTCACCTGGAAAAAAAAAAAAAAAAAAAA

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FIGURE 396

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLV
GGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSI PHPCYNSSDVEDHNNHDLMLLQL
RDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYP
GQITDGMVCAGSSKGADTCQGDSSGGLVCDGALQGITSWGS DPCGRSDKPGVYTNICRYLDWI
KKIIGSKG

Important Features:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

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FIGURE 395

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAGG
CTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAATC
AGTAGGTGACCCCGCCCCTGGATTCTGGAAGACCTCACCATGGGGACGCCCCCGACCTCGTGCG
GCCAAGACGTGGATGTTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGCACAG
GAGGACAAGGTGCTGGGGGGTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGGCCTTG
TTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCTTGTAGGTGGCAACTGGGTCCTTACAGCT
GGCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAATAAAGAT
GGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACAGCAGCGAT
GTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCCCTGGGGTCC
AAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTGCACCGTCTCA
GGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTTCCTGACACTCTCAACTGTGCAGAAGTA
AAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACAGATGGCATGGTC
TGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGGCCCCCTGGTGTGT
GATGGTGCCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGAGGTCCGACAAACCT
GGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATCATAGGCAGCAAGGGC
TGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACCTCTCTGGTTC

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FIGURE 394

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQAG
AAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFVLTATGDLALIHVEIQVL
DINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVIVGPD
ETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSNDNSPAFAESSLALE
IQEDAAPGTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPLDYEKN
PAYEVDVQARDLGPNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSFIALVMA
DDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQDQGLQPLS
AKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVSYRIQDSPV
AHLVAIDSNTGEVTAQRSLNYYEEMAGFEFQVIAEDSGQPMLASSVSVVWSLLDANDNAPEVVQ
PVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLTTIVARDADSGA
NGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGSPLQTRALLRV
MFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEKKDNRAYNCREAE
STYRQQPKRPQKHIQKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEAGWDPCLOAPFHLT
PTLYRTLNRNQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENLNLPQPATGQPRSRPLKV
AGSPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQILRSLVRLSVAFAE
RNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKEGSRSAIPDTDGPSARAGG
QTDPEQEEGPLDPEEDLSVKQLLEELSSLLDPSTGLALDRLSAPDPAWMARLSLPLTTNYRD
NVISPDAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSLLEMLLEQRSSMPVEAASE
ALRRLSVCGRTLSLDLATSAAAGMKVQGDPPGGKTGTGEGKSRGSSSSSRCL

Important features:**Signal peptide:**

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

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FIGURE 393

GTCCACATCCTGCTCAACTGGGTCAGGTCCCTCTTAGACCAGCTCTTGTCATCATTGCTGAAGTGGACCAAC
TAGTTCCCCAGTAGGGGGTCTCCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA
TGGCCTTGCCCTTGGGGTCTGCTTGTTCATAATCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGG
AAGGAGCACGGGGCTGATCAAGCCATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAACTCTAGTGGTT
TCTGAATCTAGCCCACTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG
CTACTTATTTCTTTTAGGGGATTGTGAGGAGGTGACCACTCTCACGGTGAAATACCAAGTGTGAGAGGAAGTGCC
ATCTGGTACAGTGATCGGGAAGCTGTCCAGGAACTGGGCGGGGAGGAGAGGCGGAGGCAAGCTGGGGCCGCCTT
CCAGGTGTTGCAGCTGCCTCAGGCGCTCCCCATTAGGTGGACTCTGAGGAAGGCTTGCTCAGCACAGGCAGGCG
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCCTGGTTTTCCTTTGATGTGCTTGCCACAGGGGATTT
GGCTCTGATCCATGTGGAGATCCAAGTGTGAGACATCAATGACCACCAGCCACGGTTTCCCAAAGGCGAGCAGGA
GCTGGAAATCTCTGAGAGCGCTCTCTGCGAACC CGGATCCCCCTGGACAGAGCTCTTGACCCAGACACAGGCC
TAACACCCTGCACACCTACACTCTGTCTCCAGTGAGCACTTTGCCTTGATGTGCTTGGGCGCTGATGAGAC
CAAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAAATCCATTCAATTTTTTGGATCTGGTGTTAACTGC
CTATGACAATGGGAACCCCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGTCTTGGACTCCAATGACAATAG
CCCTGCGTTTGTGAGAGTTCACTGGCACTGGAAATCCAAGAGATGCTGCACCTGGTACGCTTCTCATAAACT
GACCGCCACAGACCCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCCTCAGTAAGCACATGCCCTCCAGAGGT
GCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTCAATCTGCGTCGACCTCTAGACTATGAAAAGAACCC
TGCCTACGAGGTGGATGTTGAGGCAAGGGACCTGGGTCCCAATCCTATCCAGCCCATTCGAAAGTTCTCATCAA
GGTTCTGGATGTCAATGACAACATCCCAAGCATCCACGTCACATGGGCCTCCAGCCATCACTGGTGTCAGAAGC
TCTTCCCAAGGACAGTTTTATTGCTCTTGTCTGATGGCAGATGACTTGGATTGAGGACACAATGGTTTGGTCCACTG
CTGGCTGAGCCAAAGAGCTGGGCCACTTCAGGCTGAAAGAACTAATGGCAACACATACATGTTGCTAACCATGC
CACACTGGACAGAGAGCAGTGGCCCAATATACCCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC
AGCCAAGAAACAGCTCAGCATTGATCAGTGACATCAACGACAATGCACCTGTGTTTGAGAAAAGCAGGTATGA
AGTCTCCACGCGGGAAAACAACCTTACCCTCTCTTACCTCATTACCATCAAGGCTCATGATGCAGACTTGGGCAT
TAATGGAAAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA
GGTCACTGCTCAGAGGTCAGTGAATGAGAGATGGCCGGCTTTGAGTTCCAGGTGATCGCAGAGGACAGCGG
GCAACCCATGCTTGCATCCAGTGCTCTGTGTGGGTGAGCCTCTTGGATGCCAATGATAATGCCCGCAGGTCGGT
CCAGCCTGTGCTCAGCGATGGAAAAGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGCC
CATCGAGACTCCCAATGGCTTGGGCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGGCCATT
CCTTTTGACAACCATTTGTGGCAAGAGATGCAGACTCGGGGGCAAATGGAGAGCCCCCTCTACAGCATCCGCAATGG
AAATGAAGCCCACCTCTTCATCCTCAACCCTCATACGGGGCAGCTGTTGTCATGTACCAATGCCAGCAGCCT
CATTGGGAGTGAGTGGGAGCTGGAGATAGTAGAGGACAGGGAAGCCCCCCTTACAGACCCGAGCCCTGTT
GAGGGTCATGTTTGTCAACAGTGTGGACCACCTGAGGCACTGAGCCCGCAAGCCTGGGGCCTTGAGCATGTCTGAT
GCTGACGGTGATCTGCCTGGCTGTACTGTTGGGCATCTTCGGGTTGATCCTGGCTTTGTTTATGTCCATCTGCCG
GACAGAAAAGAAGGACAACAGGGCCTACAACCTGTGCGGAGGCGGAGTCCACCTACCGCCAGCAGCCCAAGAGGCC
CCAGAAACACATTCAGAAGGCAGACATCCACCTCGTGCCTGTGCTCAGGGGTGAGGCAGGTGAGCCTTGTGAAGT
CGGGCAGTCCCACAAAGATGTGGACAAGGAGGCGATGATGGAAGCAGGCTGGGACCCCTGCCTGCAGGCCCTT
CCACCTCACCCCGACCCGTACAGGACGCTGCGTAATCAAGGCAAGGAGCAGCCGGGAGAGCCGAGAGGT
GCTGCAAGACACGGTCAACCTCCTTTTCAACCATCCCAGGCAAGCAAGGATGCCTCCCGGAGACTGAACCTTCC
CGAGCCCCAGCCTGCCACAGGCCAGCCACGTTCCAGGCCTCTGAAGGTTGCAGGCAGCCCCACAGGGAGGCTGGC
TGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCACCAGCCTCCTCTGCAACCCTGAGACGGCAGCGACATCT
CAATGGCAAAGTGTCCTTGAGAAAGAATCAGGGCCCCGTGAGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGC
TGCCTTTCGCGGAGCGGAACCCCGTGGAGGAGCTCACTGTGATTCTCCTCCTGTTTCAAGCAATCTCCAGCTGCT
GTCCTTGCTGCATCAGGGCCAATTCCAGCCCCAACCACCAAGGAGGCTGGAGGCCAGACAGACCCAGAACAGGAGGA
CAGCAGGAGTGCAATCCAGACACAGATGGCCCAAGTGCAAGGCTGGAGGCCAGACAGACCCAGAACAGGAGGA
AGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGAAGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCC
CAGCACAGGTCTGGCCCTGGACCGGTGAGCGCCCTGACCCGGCCTGGATGGCGAGACTCTCTTTGCCCTCAC
CACCAACTACCGTGACAATGTGATCTCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGTTCCG
CAAGGCAGAGGCACAGAGCTGAGCCCAACAGGCAGGAGGCTGGCCAGCACCTTTGTCTCGGAGATGAGCTCACT
GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCGTGGAGGCCGCTCCGAGGCGCTGCGGGCGCTCTCGGT
CTGCGGGAGGACCCCTCAGTTTAGACTTGGCCACCAGTGCAGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGG
AAAGACGGGGACTGAGGGCAAGAGCAGAGGCAGCAGCAGCAGCAGGAGTGCCTGTGAACATACCTCAGACGCCT
CTGGATCCAAGAACCAGGGCCTGAGGATCTGTGGACAAGAGCTGGTTTCTAAAATCTTGTAACTCACTAGCTAG
CGGCGGCCTGAGAACTTTAGGGTGACTGATGCTACCCCCACAGAGGAGGCAAGAGCCCCAGGACTAACAGCTGAC
TGACCAAGACAGCCCTTGTAAAGCAGCTCTGAGTCTTTTGGAGGACAGGGACGGTTTGTGGCTGAGATAAGTGTT
TCTTGGCAAAACATATGTGGAGCACAAAGGGTCAGTCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGG
AAAGGGTGGCCTTCTTGGGTAGCAGGAGTCAGGGGCTGTACCCTGGGGGTGCCAGGAAATGCTCTCTGACCTAT
CAATAAGGAAAAGCAGTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 392

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPPLPA
GPGEWERRPQEPRPPKRATKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDDHVR
VAREDEVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCAGR
DLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIFEGNS
EKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTTTDDLD
FKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEFHYIAGA
HGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGGSELGGWS
LGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLENATVAAETRAVIAW
MEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSASTHRLMTDARR
RVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHESQLPEEWENNR
ESLIVFMEQVHRGIKGLVRDSHGKGIPTNAIISVEGINHDIRTANDGDYWRLLNPGEYVVTAKA
EGFTASTKNCMVGYDMGATRCDFTLSTKNMARIREIMEKFGKQPVSLPARRLLKLRGRKRRQRG

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FIGURE 391

GGGGGCTTTCTTGGGCTTGGCTGCTTGGAAACCTGCCTCCAAGGACCGGCCTCGGAGGGGTGCGCCGGGAAAGGG
AGGGAAGAAGGAAGGGCGGGGCGGGCCCCCTGCGCCCCGCGCCCTCTGCGCGCCCCCTGTCCGCCCCGGCCC
AGCCCAGCCCAGCCCCGCGGGCCGGTCAACACGCGAGCCAGCCGGCCGCTCCCGCGCCCCAAGCGCGCCGCTCTG
CTGTGCCCTGCGCCCTTGCCCCGCGCCAGCTTCTGCGCCCCGAGCCCCCGCGCCCGGCGCCCCGGTGACCGTGACCC
GCCCTGGGCGCGGGGCGGAGCAGGCATGTCCCCCGGGGACCGCTACCCAGCGCTGGCCCTGGTGCTCCTGGC
AGTGACCCTGGCCGGGGTGGAGCCCAGGGCGCAGCCCTCGAGGACCCTGATTATTACGGGCAGGAGATCTGGAG
CCGGGAGCCCTACTACGCGCGCCCGGAGCCCGAGCTCGAGACCTTCTCTCCGCGCTGCCTGCGGGGCCCCGGGA
GGAGTGGGAGCGGCGCCCGCAGGAGCCCAGGCCGCCAAGAGGGCCACCAAGCCCAAGAAAGCTCCCAAGAGGGA
GAAGTCGGCTCCGGAGCCGCTCCACCAGGTAACACAGCAACAAAAAGTTATGAGAACCAAGAGCTCTGAGAA
GGCTGCCAACGATGATCACAGTGTCCGTGTGGCCCGTGAAGATGTCAGAGAGAGTTGCCACCTCTTGGTCTGGA
AACCTTAAAAATCACAGACTTCCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCCTGGGGGCACATCGAGGGAG
ACTCAACATCCAGGCGGGCATTAAATGAAAATGATTTTTATGACGGAGCGTGGTGCAGGGGAAGAAATGACCTCCA
GCAGTGGATTGAAGTGGATGCTCGGCGCCTGACCAGATTCACTGGTGTCTCACTCAAGGGAGGAACCTCCCTCTG
GCTGAGTGAAGTGGGAGTCTTATAAGGTGATGGTGAAGCAATGACAGCCACACGTGGGTCACTGTGAAGAATGG
ATCTGGAGACATGATATTTGAGGGAAACAGTGAGAAGGAGATCCCTGTTCTCAATGAGCTACCCGTCCCATGGT
GGCCCGCTACATCCGCATAAACCCCTCAGTCCTGGTTTGATAATGGGAGCATCTGCATGAGAATGGAGATGGG
CTGCCCCTGCCAGATCCTAATAATTATTATCACCGCCGGAACGAGATGACCACCACTGATGACCTGGATTTTAA
GCACCACAATTATAAGGAAATGCGCCAGTTGATGAAAGTTGTGAATGAAATGTGTCCCAATATCACCAGAATTTA
CAACATTGGAAAAAGCCACAGGGCCCTGAAGCTGTATGCTGTGGAGATCTCAGATCACCCCTGGGGAGCATGAAGT
CGGTGAGCCCGAGTTCCACTACATCGCGGGGGCCACGGCAATGAGGTGCTGGGCGGGAGCTGCTGCTGCTGCT
GGTGCAGTTCGTGTGTGTCAGGAGTACTTGGCCGGAATGCGCGCATCGTCCACCTGGTGGAGGAGACGCGGATTCA
CGTCTCCCTCCCTCAACCCCGATGGCTACGAGAAGGCCCTACGAAGGGGGCTCGGAGCTGGGAGGCTGGTCCCT
GGGACGCTGGACCCACGATGGAATTGACATCAACAACAACCTTTCTGATTTAAACACGCTGCTCTGGGAGGCAGA
GGATCGACAGAATGTCCCAGGAAAGTTCCCAATCACTATATTGCAATCCCTGAGTGGTTTCTGTGCGAAAATGC
CACGGTGGCTGCCGAGACCAGAGCAGTCAAGCCCTGGATGGAAAAAATCCCTTTTGTGCTGGGCGGCAACCTGCA
GGGCGGCGAGCTGGTGGTGGCGTATCCCTACGACCTGGTGGCGTCCCCCTGGAAGACGCAGGAACACACCCCCAC
CCCCGATGACCACGTGTTCCGCTGGCTGGCCTACTCCTATGCCTCCACACACCGCCTCATGACAGACGCCGGAG
GAGGTGTGCCACACGGAGGACTTCCAGAAGGAGGAGGGGAGCCTGCTCAATGGGGCCTCCTGGCACACCGTCTGG
AAGTCTGAACGATTTAGCTACCTTCATACAACTGCTTGAAGTGTCCATCTACGTGGGCTGTGATAAATACCC
ACATGAGAGCCAGCTGCCCAGGAGTGGGAGAATAACCGGGAATCTCTGATCGTGTTCATGGAGCAGGTTTCATCG
TGGCATTAAAGGCTTGGTGAAGATTCACATGGAAAAGGAATCCCAACGCCATTATCTCCGTAGAAGGCATTAA
CCATGACATCCGAACAGCCAACGATGGGGATTACTGGCGCCTCCTGAACCCCTGGAGAGTATGTGGTACAGCAAA
GGCCGAAGGTTTCACTGCATCCACCAAGAACTGTATGGTTGGCTATGACATGGGGGCCACAAGGTGTGACTTCAC
ACTTAGCAAAACCAACATGGCCAGGATCCGAGAGATCATGGAGAAGTTTGGGAAGCAGCCCGTCAGCCTGCCAGC
CAGGCGGCTGAAGCTGCGGGGGCGGAAGAGACGACAGCGTGGGTGAACCCCTCCTGGGCCCCCTGAGACTCGTCTGGG
ACCCATGCAAATTAACCAACCTGGTAGTAGCTCCATAGTGGACTCACTCACTGTTGTTTCTCTGTAATTCAAG
AAGTGCCTGGAAGAGAGGGTGCATTGTGAGGCAGGTCCCAAAGGGAAGGCTGGAGGCTGAGGCTGTTTTCTTTT
CTTTGTTCCCATTTATCCAAATAACTTGGACAGAGCAGCAGAGAAAAGCTGATGGGAGTGAGAGAACTCAGCAAG
CCAACCTGGGAATCAGAGAGAGAAGGAGAAGGAGGGGAGCCTGTCCGTTGAGAGCCTCTGGCTGCATAGAAAAGG
ATTCTGGTGTCTCCCTGTTTGGCTGGCAGCAAGGGTCCACGTGCATTTGCAATTTGCACAGCTAAAAATTGCAG
CATTTCCCAGCTGGGCTGTCCCAAATGTTACCATTTGAGATGCTCCAGGCGTCTAAGAGAATCCACCCTCTC
TGGCCCTGGGACATTGCAAGCTGCTACAAATAAATTCTGTGTTCTTTTGACAATAGCGTCATTGCCAAGTGCACA
TCAGTGAGCCTCTGAATCTGTTTAGTCTCTTTTCAACAAAGGAGTGTGTTTCAGAAAAGGAGAGAGAGGCTGA
GATCATTGAGGAGTTTGTGGGAGCAAGCATGGAGCTTCTTGACAAATTTCTGGGTCCATAAACAACCCCCAAA
GTCCCTGCTGATCCAGTAGCCCTGGAGGTTCCCGAGGTAGGGAGAGCCAGAGGTGCCAGCCTTCTGAAGGGCCA
GAAAATTTAGCCTGGATCTCCTCTTTTACCTGCTAGGACTGGAAAGAGCCAGAAGTGGGGTGGCCTGAAGCCCTC
TCTCTGCTTGAAGTATTGCCCCTGTGTGGAATTGAGTGTCTCATGGGTTGGCCTCATATCAGCCTGGGAGTTATTT
TTGATATGTAGAATGCCAGATCTTCCAGATTAGGCTAAATGTAATGAAAACCTCTTAGGATTATCTGTGGAGCAT
CAGTTTGGGAAGAATTATTGAATTATCTTGCAAGAAAAAAGTATGTCTCACTTTTGTAAATGTTGCTGCCTCAT
TGACCTGGGAAAAATGAAAAAATAAAGCAAATGGTAAGACCCTTAAAAAATAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 390

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQKC
DHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTATRC
FDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDKNAIEALGSKEIRNMKFRSSWV
FIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCI PKERS

Important features:**Signal sequence.**

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

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FIGURE 389

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTCG
CCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCTGT
CCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCCCCA
AAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTACTCA
GCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGGAGAAC
AGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGAATGTGA
CAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAGTTTATTC
AGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCACAAGACTGA
ATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACATGAAATTCA
GGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTTCCGAAATTCAGAGAGAAA
AGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGAGATCCAGATAG
AAGGCTGCATACCCAAAGAACGAAGCTGACACTGCAGGGTCCTGAGTAAATGTGTTCTGTATA
AACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACAGCCCATATTTGAT
GAGTATTTTGGGTTTGTTGTAAACCAATGAACATTTGCTAGTTGTATCAAATCTTGGTACGCA
GTATTTTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGAACTAAAATGAATGG
AAATTCTTAAAAAAAAAA

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FIGURE 388

MSLLLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
ITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHVIL
KVLVRPSKPKCELEGELETEGSDLTLCESSSGTEPIVYYWQRIREKEGEDERLPPKSRIDYNH
PGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLIFLLV
WLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSSGSRSSRSGSSSTRSTANSASRSQ
RTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Important freatures:**Signal sequence:**

amino acids 1-16

Transmembrane domain:

amino acids 232-251

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FIGURE 387

GCGCCGGGAGCCCATCTGCCCCCAGGGGACGGGGCGCGGGGCCGGCTCCCGCCCGGCACATG
GCTGCAGCCACCTCGCGCGCACCCCGAGGCGCGCGCCAGCTCGCCCGAGGTCCGTCCGAGG
CGCCCGGCCGCCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATCGGG
ATGTCCCTCCTCCTTCTCCTCTTGCTAGTTTCCTACTATGTTGGAACCTTGGGGACTCACACT
GAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGCTTCCA
GAAAAAGACACTCTGGATATTGAATGGCTGCTCACCATAATGAAGGGAACCAAAAAGTGGTG
ATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCGAGTGGCC
TTTGCTTCCAATTTCTGCTGGCAGGAGATGCCTCCTTGAGATTGAACCTCTGAAGCCCAGTGAT
GAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCATGTCATCTTA
AAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGACAGAAGGAAGT
GACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATTACTGGCAGCGA
ATCCGAGAGAAAGAGGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATTGACTACAACCAC
CCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTACCAAGTGCACAGCA
GGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGGGAGTAAGTGTACAGTATGTACAAAGCATC
GGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCCTCTTGGTG
TGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAAATT
CGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCTCCTCTTCCTCAGGCTCT
CGGAGCTCACGCTCTGGTTCTTCCTCCACTCGCTCCACAGCAAATAGTGCCTCACGCAGCCAG
CGGACACTGTCAACTGACGCAGCACCCCAAGCCAGGGCTGGCCACCCAGGCATACAGCCTAGTG
GGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATGCTAATCTGACCAAAGCAGAA
ACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAAACGGTCT**TGA**ATTACAATGGAC
TTGACTCCCACGCTTTCTTAGGAGTCAGGGTCTTTGGACTCTTCTCGTCATTGGAGCTCAAGT
CACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCAGTGAGCATTGCACGGAACAGATT
CAGATGAGCATTTTCCTTATACAATAACCAAAAGCAAAAGGATGTAAGCTGATTCATCTGTA
AAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGGAAAGCAGGAGTCCAAATCTATTTGT
TGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTGAGGTGAATATACCTAAACTTTTAAT
GTGGGATATTTTGTATCAGTGCTTTGATTACAAATTTTCAAGAGGAAATGGGATGCTGTTTGT
AAATTTTCTATGCATTTCTGCAAACCTTATTGGATTATTAGTTATTCAGACAGTCAAGCAGAAC
CCACAGCCTTATTACACCTGTCTACACCATGTACTGAGCTAACCCTTCTAAGAACTCCAAA
AAAGGAAACATGTGTCTTCTATTCTGACTTAACCTTCATTTGTCATAAGGTTTGGATATTAATT
TCAAGGGGAGTTGAAATAGTGGGAGATGGAGAAGAGTGAATGAGTTTCTCCCACTCTATACTA
ATCTCACTATTTGTATTGAGCCCAAAATAACTATGAAAGGAGACAAAAATTTGTGACAAAGGA
TTGTGAAGAGCTTTCCATCTTCATGATGTTATGAGGATTGTTGACAAACATTAGAAATATATA
ATGGAGCAATTGTGGATTTCCCCTCAAATCAGATGCCTCTAAGGACTTTCCTGCTAGATATTT
CTGGAAGGAGAAAATACAACATGTCATTTATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAA
AAGGGATCTAGGAATGCTGAAAGATTACCCAACATACCATTATAGTCTCTTCTTTCTGAGAAA
ATGTGAAACCAGAATTGCAAGACTGGGTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTA
ATATGTCAAGGAAGGTAGCCGGGCATGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAG
GTTGCAGTGAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

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FIGURE 386

MRLLVLLWGCLLLPGYEALEGP EEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRC SG
TIYAE EEGQETMKGRVSIRD SRQELSLIVTLWNLTLQDAGEYWCGVEKRGPD E SLLISLFVFP
GPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPGTSQ
YGHERTSQYTGTSPHPATSP PAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI LAPV
LVLLSLLSAAGLIAFC SHLLLWRKEAQQTETQRNEKFWLSRLTAE E KEAPSQAPEGDVISMP
PLHTSEEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

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FIGURE 385

CTCCACGGTGTCCAGCGCCCAGAAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCTC
CCAGGTTATGAAGCCCTGGAGGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGTCC
CTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGTGGG
ATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAATGAAG
GGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGAACCTC
ACCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAGTCTTTA
CTGATCTCTCTGTTTCGTCTTTCCAGGACCCTGCTGTCCTCCCTCCCCCTTCTCCCACCTTCCAG
CCTCTGGCTACAACACGCCTGCAGCCCCAAGGCAAAAGCTCAGCAAACCCAGCCCCCAGGATTG
ACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGGGGCTGAGGGC
CCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACACAGGAACCTCT
CCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCCGCCCCCCCCATGCAGCTGGACTCCACC
TCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGGGTGTCCATCCCG
ATGGTCCGCATACTGGCCCCAGTCCTGGTGTGCTGAGCCTTCTGTGAGCCGCAGGCCTGATC
GCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCACGGAGACACAGAGG
AACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCCCCCTTCCCAGGCCCCCT
GAGGGGGACGTGATCTCGATGCCTCCCCCTCCACACATCTGAGGAGGAGCTGGGCTTCTCGAAG
TTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGTGAAGCAGTATGGCTGGC
TGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAGTCCAGCTGCCCCGACTCC
AGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGATGTTCCAGCCTGACCTAGAAGCGTTT
GTCAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTGGGAGACTGGGACATCCCTGAT
AGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCAGCAGGGCCAGACAAGGCTCAG
TGGATCTGGTCTGAGTTTCAATCTGCCAGGAACTCCTGGGCCTCATGCCCAGTGTGCGACCCCT
GCCTTCTCCTCCCACTCCAGACCCCCACCTTGTCTTCCCTCCCTGGCGTCTCAGACTTAGTCCCA
CGGTCTCCTGCATCAGCTGGTGTATGAAGAGGAGCATGCTGGGGTGAGACTGGGATTCTGGCTT
CTCTTTGAACCACCTGCATCCAGCCCTTCCAGGAAGCCTGTGAAAAACGTGATTCTTGGCCCCA
CCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAGGACTCTGAATTCTAACAATGCCCAGT
GACTGTGCACTTGAGTTTGAGGGGCCAGTGGGCCTGATGAACGCTCACACCCCTTCCAGCTTAG
AGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCCAATAGATCTGCTCTGTCTGCGACACCA
GATCCACGTGGGGACTCCCCTGAGGCCTGCTAAGTCCAGGCCTTGGTCCAGGTCCAGGTGCACAT
TGCAGGATAAGCCCAGGACCGGCACAGAAGTGGTTGCCTTTNCCATTTGCCCTCCCTGGNCCA
TGCCTTCTTGCCTTTGGAAAAAATGATGAAGAAAACCTTGGCTCCTTCCCTTGTCTGGAAAGGG
TTACTTGCCTATGGGTTCTGGTGGCTAGAGAGAAAAGTAGAAAACCAGAGTGCACGTAGGTGT
CTAACACAGAGGAGAGTAGGAACAGGGCGGATACCTGAAGGTGACTCCGAGTCCAGCCCCCTG
GAGAAGGGGTGCGGGGTGGTGGTAAAGTAGCACTACTATTTTTTTTCTTTTTTCCATTATT
ATTGTTTTTTAAGACAGAATCTCGTGCTGCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCA
AACTCCGCCTCCTGGGTTCAAGTGATTCTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAG
GCACGCACCAACACACCTGGCTAATTTTTGTACTTTTAGTAGAGATGGGGTTTCACCATGTTG
GCCAGGCTGGTCTTGAACCTCTGACCTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCG
GGATTACAGGCATGAGCCACTGTGTCTGGCCCTATTTCTTTAAAAAGTGAAATTAAGAGTTG
TTCAGTATGCAAACTTGGAAGATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCA
TAGTCTCACCAAGAGACTATCATTATTTCTGTTTTGTGTACTTCCTTCCACTCTTTTCTTCTTC
ACATAATTTGCCGGTGTCTTTTTTACAGAGCAATTATCTTGTATATACAACCTTTGTATCCTGC
CTTTTCCACCTTATCGTTCCATCACTTTATTCAGCACTTCTCTGTGTTTTTACAGACCTTTTT
ATAAATAAAATGTTTCATCAGCTGCATAAAAAAAAAAAAAA

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FIGURE 384

MRLFLWNAVLTFLFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSLF
HSTHKHNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPESTLI
FNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVEDIFD
KEDEDKDGFIAREFTYKHDEL

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

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FIGURE 383

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTCCTGAACTTGTCTG
AAGCCCTTGTCCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCGAGGGACCTTTCGCTGCTTTTGTAGGG
ACTTCTTTCCTTGCTTCAGCAACATGAGGCTTTTCTTGTGGAACGCGGTCTTGACTCTGTTCTGTCACCTTCTTTGA
TTGGGGCTTTGATCCCTGAACCAGAAGTGAAAATTGAAGTTCTCCAGAAGCCATTCATCTGCCATCGCAAGACCA
AAGGAGGGGATTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTCACA
AACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGTTGGGACCAGGGCTTGA
AAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCCTCCTGCTCTGGGCTATGGAAAAGAAGGAAAAGGTA
AAATTCCCCCAGAAGTACACTGATATTTAATATTGATCTCCTGGAGATTGCAAATGGACCAAGATCCCATGAAT
CATTCCAAGAAATGGATCTTAATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGT
TTGAAAACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAGAAGATG
AAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTATAGAGATACATCTACCCTT
TTAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAAAGAACATTTTATTTTTATACAATGTTCTTTCT
TGCTTTGTTTTTATTTTTATATATTTTTCTGACTCCTATTTAAAGAACCCTTAGGTTTCTAAGTACCCATTT
CTTTCTGATAAGTTATTGGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTTCACTTTC
ACAGATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAAATGTTGCAACTGGGAATATACCACGACATGA
GACCAGGTTATAGCACAAATTAGCACCCCTATATTTCTGCTTCCCTCTATTTTCTCCAAGTTAGAGGTCAACATTT
GAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCATGTTATAATGAAATAGTTTATGTGTAAGTGGCTCTG
AGTCTCTGCTTGAGGACCAGAGGAAAATGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGAT
GTGCAATGCTGAAGTTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGA
GGCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTTCGAGACCAGCCTGACCAACACGGAGAAACCCTATCTCTAC
TAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCCTGTAATCCCAGCTACCCAGGAAGGCTGAGGCGGCAGAA
TCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAGATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAA
AAGAACACGGTTAATACCATATNAATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGG
CTCCTAGTGATTGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATGTA
TCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGCTAGCGGAATATCCTT
CCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACATTGTATCATAAGATAAAGTAGTAAACCA
GTCTACATTTTCCCATTTCTGTCTCATCAAAAAGTGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAG
CACTTTGGGGGCCAAGGAGGGTGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCT
TGTCTCTACTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCCAGCTACTCGGGAGGGCTGA
GACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCCACTGCACTCCAGCCTGGG
TGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAGAAGCAGACCTACAGCAGCTACTATTGAATAAATACCTA
TCCTGGATTTT

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FIGURE 382

MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI F
LHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPATF
HGLGRLHTLHLDRCLQELGPGFLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHGNR
ISSVPERAFRGLHSLDRLLHQNRVAHVHHPHAFRDLGRLMTLYLFANNLSALPTEALAPLRL
QYLRLNDNPWVCDRCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQCAVATGP
YHPIWTGRATDEEPLGLPKCCQPDAAKASVLEPGRPASAGNALKGRVPPGDSPPGNGSGPRH
INDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQAGSGGGGT
GDSEGS GALPSLTCSLTPLGLALVLWTVLGPC

Important features:**Signal peptide:**

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

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FIGURE 381

GGCGCCGGTGACCGGGCGGGCTGAGCGCTCCTGCGGCCCGGGCCTGCGCGCCCCGGCCCCGCC
GCGCCGCCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCCGCGCCCCGCC
CCGCGCCCAAGGTGAGCGCTCCGCCCCGCGCGAGGCCCGCCCGGCCCGCCCCGCCCCGCC
CGGCCGGCGGGGAACCGGGCGGATTCCTCGCGCGTCAAACCACCTGATCCCATAAAACATTC
ATCCTCCCGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCGCGCCGCCCTCGCCCTG
TGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCCAGCCAGAGCCGGGCGGAGCGGAGCG
CGCCGAGCCTCGTCCCGCGGCCGGGCCGGGGCCGGGCCGTAGCGGCGGCGCCTGGATGCGGAC
CCGGCCGCGGGGAGACGGGCGCCCCGCCCGAAACGACTTTCAGTCCCCGACGCGCCCCGCCCA
ACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTGCTGTGGCTG
CAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGAGCCCAAGGTG
ACGACAAGCTGCCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTGCTGCCAGCCAG
CGCATCTTCCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTCCTGCTGCCGC
AACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCCGAATTGATGCGGCTGCCTTCACT
GGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCCGGTCTGTGGACCCT
GCCACATTCCACGGCCTGGGCCGCTACACACGCTGCACCTGGACCGCTGCGGCCTGCAGGAG
CTGGGCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTACCTGCAGGACAACGCG
CTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCACACACCTCTTCCTGCAC
GGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTGCACAGCCTCGACCGTCTC
CTACTGCACCAGAACCGCGTGGCCCATGTGCACCCGCATGCCTTCCGTGACCTTGGCCGCCTC
ATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCACTGAGGCCCTGGCCCCCCTG
CGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTGTGTGACTGCCGGGCACGCCCA
CTCTGGGCCTGGCTGCAGAAGTTCGCGGCTCCTCCTCCGAGGTGCCCTGCAGCCTCCCGCAA
CGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATGACCTGCAGGGCTGCGCTGTGGCC
ACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACCGATGAGGAGCCGCTGGGGCTTCCC
AAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGTACTGGAGCCTGGAAGACCAGCTTCG
GCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTGACAGCCCGCCGGGCAACGGCTCTGGC
CCACGGCACATCAATGACTACCCCTTGGGACTCTGCCTGGCTCTGCTGAGCCCCCGCTCACT
GCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTTCCCCACCTCGGGCCCTCGCCGGAGGCCA
GGCTGTTACGCAAGAACCGCACCCGCAGCCACTGCCGTCTGGGCCAGGCAGGCAGCGGGGT
GGCGGGACTGGTGACTCAGAAGGCTCAGGTGCCCTACCCAGCCTCACCTGCAGCCTCACCCCC
CTGGGCCTGGCGCTGGTGCTGTGGACAGTGCTTGGGCCCTGCTGAACCCCCAGCGGACACAAGA
GCGTGCTCAGCAGCCAGGTGTGTGTACATACGGGGTCTCTCTCCACGCCGCCAAGCCAGCCGG
GCGGCCGACCCGTGGGGCAGGCCAGGCCAGGTCTCCCTGATGGACGCCTGCCGCCCGCCACC
CCCATCTCCACCCCATCATGTTTACAGGGTTCGGCGGCAGCGTTTGTTCAGAACGCCGCTC
CCACCCAGATCGCGGTATATAGAGATATGCATTTTATTTTACTTGTGTAAAAATATCGGACGA
CGTGGAATAAAGAGCTCTTTTCTTAAAAAA

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FIGURE 380

MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLLS
GATATAALPLEGGPTGRDSEHMQEAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVARR
QEGAPPQQSARRDRMPCRNFFWKTFSSCK

Important features:**Transmembrane domain:**

amino acids 51-69

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 35-39, 92-96

N-myristoylation sites.

amino acids 64-70, 75-81, 90-96

Amidation site.

amino acids 33-37

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FIGURE 379

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTCACATGGGCACAA
TTTCACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCACTTGTTTTTGTT
CTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAAGTTCTCCAGAAGCAAGC
GCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCTTTAA
TTAAGGGGTTACATCCAACCCCAGAGCGCTTTTGTGGGCACTGATTGCTCCAGCTTCTGCGTC
ACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGACATGTATAGACACAAAAACAGCTG
GAGATTGGGCTTAAAATACCCACCAAGCTCCAAAGAAGAGACCCAAGTCCCCAAAACATTGAT
TTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCAGCCCACAA
GATGCCATTGTCCCCCGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCT
GCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAG
GAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAGGCCAGTGCCGG
GCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCAGCA
ATCCGCGCGCCGGGACAGAATGCCCTGCAGGAAGTTCTTCTGGAAGACCTTCTCCTCCTGCAA.
ATAG

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FIGURE 378

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRCQALYLPVHYGFHTPASDIQIIWLFERPHTMPKYLLGSVNKS
VVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIIQNGTSLASQKIQVTVDDPVTKPVVQIHPPSGAVEY
VGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFSPQNNTLHIAPVTKEDIGNYSCLVRNPVSEMEDIIIMPII
YYGPGYGLQVNSDKGLKVGCVFTVDLGEAILEDSCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMD
YVCCAYNNITGRQDETHFTVITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQKLEG
RPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTVYEVIQHIIPAQQQDHPE

Important features:**Signal sequence:**

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208, 276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237, 239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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FIGURE 377

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCTTTAGATTGTGAA
ATGTGGCTCAAGGTCTTCACAACTTTTCCTTTTCCTTTGCAACAGGTGCTTGCTCGGGGCTGAAG
GTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTCAC
TATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCACACA
ATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACCAACAC
AAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTGATGAA
GGCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAACCTCTATCTGCCAGTCAGAAGATA
CAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTGCAGATTCATCCTCCCTCTGGGGCT
GTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGGCTAGCTTAC
CAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTCTCCCCAAAC
AATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCTGCCTGGTGAGG
AACCCTGTGAGTGAAATGGAAAGTGATATCATTATGCCCATCATATATTATGGACCTTATGGA
CTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGTTGACCTTGGAGAG
GCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACTCCTGGATTAGGAGG
ACTGACAATACTACATATATCATTAAAGCATGGGCCTCGCTTAGAAGTTGCATCTGAGAAAGTA
GCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAACCGGCAGGCAAGATGAA
ACTCATTTTCAGATTATCATCACTTCCGTAGGACTGGAGAAGCTTGCACAGAAAGGAAAATCA
TTGTCACCTTTAGCAAGTATAACTGGAATATCACTATTTTTTGATTATATCCATGTGTCTTCTC
TTCCTATGGAAAAAATATCAACCCTACAAAGTTATAAAACAGAACTAGAAGGCAGGCCAGAA
ACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATGCTCTGGATGACTTCGGAATA
TATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGGATTCCAAGCAGGTCTGTTCCA
GCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGTGTATGAAGTTATTCAGCACATC
CCTGCCCAGCAGCAAGACCATCCAGAGTGAACTTTTCATGGGCTAAACAGTACATTCGAGTGAA
ATTCTGAAGAAACATTTTAAAGGAAAAACAGTGGAAAAGTATATTAATCTGGAATCAGTGAAGA
AACCAGGACCAACACCTCTTACTCATTATTCCTTTACATGCAGAATAGAGGCATTTATGCAAA
TTGAACTGCAGGTTTTTTCAGCATATACACAATGTCTTGTGCAACAGAAAAACATGTTGGGGAA
ATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGGGGAGAACGAAAGTGACAGGGGTTTCCT
CATAAGTTTTGTATGAAATATCTCTACAAACCTCAATTAGTTCTACTCTACACTTTCCTATC
ATCAACACTGAGACTATCCTGTCTCACCTACAAATGTGGAACTTTACATTGTTTCGATTTTTT
AGCAGACTTTGTTTTATTAAATTTTTATTAGTGTTAAGAATGCTAAATTTATGTTTCAATTTT
ATTTCCAAATTTCTATCTTGTTATTTGTACAACAAAGTAATAAGGATGGTTGTCACAAAAACA
AACTATGCCTTCTCTTTTTTTTCAATCACCAGTAGTATTTTTGAGAAGACTTGTGAACACTT
AAGGAAATGACTATTAAAGTCTTATTTTTTATTTTTTTCAAGGAAAGATGGATTCAAATAAATT
ATTCTGTTTTTGCTTTTTAAAAA

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FIGURE 376

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMDNVTVRQGESATLRCTIDNRV
TRVAWLNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTDNHPKTS
RVHLIVQVSPKIVEISSDISINEGNNISLT CIATGRPEPTVTWRHISPKAVGVSEDEYLEIQ
GITREQSGDYEC SASNDVAAPVVR RVKVTVNYPPISEAKGTGVPVGQKGT LQCEASAVPSAE
FQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGN YTCVASNKLGHTNASIMLFGPGA
VSEVSNGTSRRAGCVWLLPLLVLHLLLKF

Important features:**Signal peptide:**

amino acids 1-28

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FIGURE 375

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAAT
CTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGAAA
AAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGG
GCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAA
AGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAA
CCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTG
GTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCA
GAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA
GACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAATTTGTAGAGATTTCTTCAGATAT
CTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTAC
GGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA
AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGC
CGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACATCCACCATAACATTTCAGAAGCCAA
GGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTC
AGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGT
GGAAAACAGACCTTTTCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAA
CTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCC
AGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCC
TCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGAATGTGAGTGCCACTTCCCCACCCGGGAAAG
GCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA
TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAACAAA
GAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATATTTAGG
TACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGACCCACTGCA
AGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCCACAGA
GTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAA
CAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCACCACG
GCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAA

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FIGURE 374

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERMELSKSFRVYCIILV
KPKDVS LWA AVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKYAFDKYRDQYNWFFLARPTTFAI
IENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAV
CLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFG
HIFNDALVFLPPNGSDND

Important features:**Signal sequence:**

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389, 399-403,
409-413, 473-477, 729-733, 748-752**Tyrosine kinase phosphorylation site.**

amino acids 736-743

N-myristoylation site.amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550, 558-564,
651-657, 657-663, 672-672**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

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FIGURE 373

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCCG
TTCTAGACGCGGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGAA
GCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAATGC
ACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTTCAGAGG
ATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAACCCCAAAG
ATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAGAGTTCT
TCAGTTCTGAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATGTGGTTAA
TGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACTGGTTCTTCC
TTGCACGCCCCACTACGTTTGCTATCATTTGAAAACCTAAAGTATTTTTTGTAAAAAAGGATC
CATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATATGTGGGTATGG
AAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCTCAATATCCCAG
AAAAGTGTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAACAGCTAGCAGTTT
GCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGAAAAGATGTATTTA
ATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCCCAACCAGGTAGTAG
AAGGCTGTTGTTTCAGATATGGCTGTTACTTTTAATGGACTGACTCCAAATCAGATGCATGTGA
TGATGTATGGGGTATACCGCCTTAGGGCATTGCGGCATATTTTCAATGATGCATTGGTTTTCT
TACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCGTGAATATGATCTTTGTA
TAGGACGTGTGTTGTCATTATTTGTAGTAGTAACACTACATATCCAATACAGCTGTATGTTTCTT
TTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAGTCAGTAGTACATTTTTTAA
TGAGGGTGGTTTTTTTTCTTTAAACACATGAACATTGTAAATGTGTTGGAAAGAAGTGTTTTA
AGAATAATAATTTTGCAAATAAACTATTAATAAATATTATATGTGATAAATTCTAAATTATGA
ACATTAGAAATCTGTGGGGCACATATTTTTGCTGATTGGTTAAAAAATTTTAACAGGTCTTTA
GCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATTTGTGATTAAAGTAAAACCTTTTAG
CTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCTAAGCCTCCCCAAGTTCCAATGGAT
TTGCCTTCTCAAATGTACAATAAGCAACTAAAGAAAATTAAAGTGAAAGTTGAAAAAT

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FIGURE 372

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRPS
QDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGHTG
PKGQKGSMPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFYCYV
PGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWVRLYK
GERENAI FSEELDTYITFSGYLVKHATEP

Important features:**Signal sequence.**

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

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FIGURE 371

CAC TTT TCT C C C T C T C T T T A C T T T T C G A G A A A C C G C G C T T C C G C T T C T G G T C G C A G A G A C C T C G G A G A C C G C G
C C G G G G A G A C G G A G G T G C T G T G G G T G G G G G G A C C T G T G G C T G C T C G T A C C G C C C C C A C C C T C C T C T T C T G C A C
T G C C G T C C T C C G G A A G A C C T T T T C C C C T G C T C T G T T T C C T T C A C C G A G T C T G T G C A T C G C C C C G G A C C T G G C C G G
G A G G A G C T T G G C C G G C G G G A G A T G C T C T A G G G G C G G C G G G A G G A G C G G C C G G C G G G A C G G A G G G C C C G G C A G
G A A G A T G G G C T C C C G T G G A C A G G G A C T C T T G C T G G C G T A C T G C C T G C T C C T T G C C T T G C C T C T G G C C T G G T C C T
G A G T C G T G T G C C C C A T G T C C A G G G G A A C A G C A G G A G T G G G A G G G A C T G A G G A G C T G C C G T C G C C T C C G G A C C A
T G C C G A G A G G G C T G A A G A A C A C A T G A A A A T A C A G G C C C A G T C A G G A C C A G G G G C T C C C T G C T T C C C G G T G C T T
G C G C T G C T G T G A C C C C G T A C C T C C A T G T A C C C G G C G A C C G C T G C C C C A G A T C A A C A T C A C T A T C T T G A A A G G
G G A G A A G G G T G A C C G C G G A G A T C G A G G C C T C C A A G G G A A A T A T G G C A A A C A G G C T C A G C A G G G G C C A G G G G C C A
C A C T G G A C C C A A A G G G C A G A A G G G C T C C A T G G G G G C C C C T G G G G A G C G G T G C A A G A G C C A C T A C G C C G C C T T T T C
G G T G G G C C G G A A G A A G C C C A T G C A C A G C A A C C A C T A C T A C C A G A C G G T G A T C T T C G A C A C G G A G T T C G T G A A C C T
C T A C G A C C A C T T C A A C A T G T T C A C C G G C A A G T T C T A C T G C T A C G T G C C C G G C C T C T A C T T C T T C A G C C T C A A C G T
G C A C A C C T G G A A C C A G A A G G A G A C C T A C C T G C A C A T C A T G A A G A A C G A G G A G G A G G T G G T G A T C T T G T T C G C G C A
G G T G G G C G A C C G C A G C A T C A T G C A A G C C A G A G C C T G A T G C T G A G C T G C G A G A G C A G G A C C A G G T G T G G G T A C G
C C T C T A C A A G G G C G A A C G T G A G A A C G C C A T C T T C A G C G A G G A G C T G G A C A C C T A C A T C A C C T T C A G T G G G T A C C T
G G T C A A G C A C G C C A C C G A G C C C T A G C T G G C C G G C C A C C T C C T T T C C T C T C G C C A C C T T C A C C C C T G C G C T G T G C
T G A C C C C A C C G C C T C T T C C C C G A T C C C T G G A C T C C G A C T C C C T G G C T T T G G C A T T C A G T G A G A C G C C C T G C A C A C
A C A G A A G C C A A A G C G A T C G G T G C T C C C A G A T C C C G C A G C C T C T G G A G A G A G C T G A C G G C A G A T G A A A T C A C C A G
G G C G G G C A C C C G C G A G A A C C C T C T G G G A C C T T C C G C G G C C C T C T C T G C A C A C A T C C T C A A G T G A C C C C G C A C G G
C G A G A C G C G G G T G G C G G C A G G G C G T C C C A G G G T G C G G C A C C G C G G C T C C A G T C C T T G G A A A T A A T T A G G C A A A T T
C T A A A G G T C T C A A A A G G A G C A A A G T A A A C C G T G G A G G A C A A A G A A A A G G G T T G T T A T T T T T G T C T T T C A G C C A G
C C T G C T G G C T C C C A A G A G A G A G G C C T T T T C A G T T G A G A C T C T G C T T A A G A G A A G A T C C A A A G T T A A A G C T C T G G G
G T C A G G G G A G G G G C C G G G G C A G G A A A C T A C C T C T G G C T T A A T T C T T T T A A G C C A C G T A G G A A C T T T C T T G A G G G
A T A G G T G G A C C C T G A C A T C C C T G T G G C C T T G C C A A G G G C T C T G C T G G T C T T T C T G A G T C A C A G C T G C G A G G T G A
T G G G G G C T G G G G C C C A G G C G T C A G C C T C C C A G A G G G A C A G C T G A G C C C C C T G C C T T G G C T C C A G G T T G G T A G A A
G C A G C C G A A G G G C T C C T G A C A G T G G C C A G G G A C C C C T G G G T C C C C C A G G C C T G C A G A T G T T T C T A T A G A G G G C A G
A G C T C C T T G G T A C A T C C A T G T G T G G C T C T G C T C C A C C C C T G T G C C A C C C C A G A G C C C T G G G G G G T G G T C T C C A T G
C C T G C C A C C C T G G C A T C G G C T T T C T G T G C C G C C T C C C A C A A A T C A G C C C C A G A A G G C C C C G G G G C C T T G G C T T
C T G T T T T T T A T A A A A C A C C T C A A G C A G C A C T G C A G T C T C C C A T C T C C T C G T G G G C T A A G C A T C A C C G C T T C C A C G
T G T G T T G T G T T G G T T G G C A G C A A G G C T G A T C C A G A C C C C T T C T G C C C C C A C T G C C C T C A T C C A G G C C T C T G A C C A
G T A G C C T G A G A G G G C T T T T T C T A G G C T T C A G A C A G G G G A G A G C T G G A A G G G G C T A G A A A G C T C C C G C T T G T C T
G T T T C T C A G G C T C C T G T G A G C C T C A G T C C T G A G A C C A G A G T C A A G A G G A A G T A C A C G T C C C A A T C A C C C G T G T C A
G G A T T C A C T C T C A G G A G C T G G G T G G C A G G A G A G G C A A T A G C C C C T G T G G C A A T T G C A G G A C C A G C T G G A G C A G G G
T T G C G G T G T C T C C A C G G T G C T C T G C C C T G C C C A T G G C C A C C C C A G A C T C T G A T C T C C A G G A A C C C C A T A G C C C C
T C T C C A C C T C A C C C C A T G T T G A T G C C C A G G G T C A C T C T T G C T A C C C G C T G G G C C C C A A C C C C C G C T G C C T C T C
T T C C T T C C C C C A T C C C C C A C C T G G T T T T G A C T A A T C C T G C T T C C C T C T C T G G G C C T G G C T G C C G G G A T C T G G G G
T C C T A A G T C C C T C T C T T T A A G A A C T T C T G C G G G T C A G A C T C T G A A G C C G A G T T G C T G T G G G C G T G C C C G G A A G
C A G A G C G C A C A C T C G C T G C T T A A G C T C C C C C A G C T C T T C C A G A A A C A T T A A A C T C A G A A T T G T G T T T C A A

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FIGURE 370

MEGEEAEQPAWFHQWPWPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS
GHSLSPEENEFAEEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLPEH
TNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNKLT
APRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNVEVLI
LSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDNETFWK
LSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSDANVLTPIRSLEYLLLHSNQLREQG
IHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMLHNQITGIGREDFATTYFLEELNLS
YNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALARGALAGMA
QLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYLQNNKISAVP
ANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKEE
EEEEEEEEEEETR

Important features:**Signal sequence:**

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554**Leucine zipper pattern.**amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

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FIGURE 369

CAAAACCTTGCGTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC
TGGGGGAGCGCGTTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCTGGGTGGTCCCGTCCCTATCCCTCCTTTATATA
GAAACCTTCCACACTGGGAAGGCAGCGGCGAGGCAGGAGGGCTCATGGTGAGCAAGGAGGCCGGCTGATCTGCAG
GCGCACAGCATTCCGAGTTTACAGATTTTACAGATACCA**AATGGA**AGGCGAGGAGGCAGAACAGCCTGCCTGGT
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCCAGAGCCGGGTGCTGC
TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGCCGTGAGGGCCCCAGGATTTGGCCGAA
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTTGCGGAGGAGGAGCCGGTGTGGTACTGAGCCCTGAGG
AGCCCGGGCCTGGCCCAGCCGCGGTGAGCTGCCCCCGAGACTGTGCCTGTTCCAGGAGGGCGTCTGTGGACTGTG
GCGGTATTGACCTGCGTGAGTTCCTGGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAGAACCAACCAGC
TGGAAGATCTACCCTGAGGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAAACAACCGCCTGA
CTTCCCGAGGGCTCCAGAGAAGGCGTTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC
TGACCTTGGCACCCCGCTTCCTGCCAAACGCCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCT
ATGGGCTCACCTTTGGCCAGAAGCCAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGGC
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCATCCTGTCCAGCAACTTCCTGCGCCACGTGC
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGGGGGCCT
TCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAACAACTACCTGACTGACGAGGGCCTGGACAACGAGA
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGC
CGCGCAGCCTGGTGTGCTGCTGCACTTGGAAGAAGACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCATCC
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACAGCTGCGGGAGCAGGGCATCCACCCACTGGCCTTCAGGGCC
TCAAGCGGTGTCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCTGCCAGTGGCCTGCCCTGCGCCGCTGC
GCACCCTCATGATCCTGCACAACCAGATCACAGGCATTGGCCGCGAAGACTTTGCCACCACCTACTTCCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACAGCCACAGGTGCACCGCGACGCTTCGCAAGCTGCGCCTGCTGC
GCTCGCTGGACCTGTGCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCTTGGCACGAGGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCGTGCCTGGGTGGACCTCGCCCATCTGCAGCTGCTGGACA
TCGCGGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACAA
AGATTAGTGCGGTGCCCCGCAATGCCTTCGACTCCACGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAACAAGC
TGGCTGTGGGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGACATTGAAGGCAACT
TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGGAAGGAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAAGAT**TAGT**GACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGGACTCTTTTCTGC
AGCACACGCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA
TCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCACGGCGTGTCCACGGCCAGACACATGC
ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACACAACCTACCTCCAAACCACACAGTCTCTGTACAC
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGGTCTGCCCTGCCCTGGCACACACAGGCACCCA
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACCACACACACACATGCACAAGTCATGTGCGAA
CAGCCCTCCAAAGCCTATGCCACAGACAGCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCT
GTCCATCTGTCCGTCCGTTCCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCCTCT
GGAACCTCACAAAAGCTGGCTTTTATTCCTTTCCCATCCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGCC
TGGCCACCCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACTTTTCCAATGGGCAAGCCAGTGGAGGCAGGATGGGAGAGCCCTGGGTGCTGCTGGGGCCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTTT
GTTCTTCAGGCCTGTGGGGGAAGTCCGGGTGCCTTTATTTTTTATTCTTTCTAAGGAAAAAATGATAAAAT
CTCAAAGCTGATTTTCTTGTATAGAAAACTAATATAAAGCATTATCCCTATCCCTGCAAAAAA

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FIGURE 368

MLNKMTLHPQQIMIGPRFNRAFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVICVRKNLREVPDGIS
TNTRLLNLHENQIQIIVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKL
KELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDLDEL
LSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNADFNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLH
NPWNCNCDILWLSWWIKDAPSNNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKC
RASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVNSVGNNTASATLNVTAATTP
FSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQSTRSTEKFTTIPVTDINSGIPGIDEVMKT
TKIIIGCFVAITLMAAVMLVIFYKMRKQHRQNHHAHPTRTVEIINVDEITGDTPMESHLPMIPAIEHEHLNHYS
YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

Important features:**Signal sequence:**

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438, 442-446,
488-492, 606-610**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243, 391-397,
422-428, 433-439, 531-537

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FIGURE 367

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG
AAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTTAGACCCGCGGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCCTCC
CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTACAAAAGAAAAAGTATGTTTCATTTTTCTC
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAAAGAACT
GGTGTGGTGGTGTGTTTTCTTTCTTTTGAATTTCCACAAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTTTTTTTAAAT
TTTTATTCCTTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACCACCTGGATTTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACCTGTTTGAATTCAGAAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAACAGGGCCCTATTTGACCCCTGCTTGTGGTGTCT
GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCAGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA
CCAGTTTCAAGGATGATTTGTGTTTCGGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAATCCT
ACAGTTGATAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTT
GCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAACAGAATTCTTCTTTGCGCCGACTAGACTTAGG
GGAATTGAAAAGACTTTTCATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAATTGAGGTATTTGAACCTTGC
CATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACCTAGATGAGCTGGATCTTTCTGGGAATCA
TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAACCTGTGGATGATACAGTCCAGAT
TCAAGTGATTGAACGGAATGCCTTTGACAACCTTCACTGCTAGTGGAGATCAACCTGGGCACACAATAATCTAAC
ATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACATTTACATCACAACCTTGGAACCTG
TAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTTGTGCCCGGTG
TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTGGGGCTCCACATC
CCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGT
GCTCAGTGATGGTACGTTAAATTTACAAATGTAACCTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCCTTTCTTACTTTTC
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCCCTCC
AGTGGTCGACTGGGAGACCACCAATGTGACCACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTT
CACCATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT
TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGATGAGGAAGCAGCACC
TCGGCAAAACCATCACGCCCCAACAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC
CATGGAAGGCCACCTGCCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT
CAACCACACAACAACAGTTAACACAATAAATTCATACACAGTTTCACTGATGAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAAACAATCAAAAAA
GACAGTTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAA
AAAAGAAAAGAAATTTATTTATTAAAAATCTATTGTGATCTAAAGCAGACAAAAA

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FIGURE 366

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLS CAYSGFSSPRVEWK
FDQGD TTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKVKL
IVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYV
LNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVTLLILGI
LVFGIWFAYS RGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Important features:**Signal sequence:**

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

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FIGURE 365

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGACAAAG
GCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGGCA
TTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCTGTG
AAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCAAGGA
GACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGGTGACC
TTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATACACTTGT
ATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGTGCTTGTG
CCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGGGCAGTGCTG
ACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGATGGGATAGTG
ATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACA
ACAGGAGAGCTGGTCTTTGATCCCCCTGTCAGCCTCTGATACTGGAGAATACAGCTGTGAGGCA
CGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAAT
GTGGGGGTATCGTGCGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAATCTTGTTTGGC
ATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAGAAAGGGACTTCGAGTAAGAAG
GTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCTG
GTGTGAGCCTGGTTCGGCTCACCGCCTATCATCTGCATTTGCCTTACTCAGGTGCTACCGGACT
CTGGCCCCCTGATGTCTGTAGTTTACAGGATGCCTTATTTGTCTTCTACACCCACAGGGCCC
CCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCCATCCTCCTTCATGCCCTC
CCTCCCTTTCCTACCACTGCTGAGTGGCCTGGAACCTTGTTTAAAGTGTTTATTCCTTCT
TTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCCTTCTAAGTAGACAGCAAAAA
TGGCGGGGGTTCGAGGAATCTGCACTCAACTGCCACCTGGCTGGCAGGGATCTTTGAATAGG
TATCTTGAGCTTGTTCTGGGCTCTTTCCTTGTGTACTGACGACCAGGGCCAGCTGTTCTAGA
GCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGGTGATGACACTGGGGTCCTTCCAT
CTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTGCCACTGGGATCCCTCTGCCCTGTC
CTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGTGGAAAATGGGAGCTCTTGTTGTGGA
GAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAGGATTTAAAACCGCTGCTCTAAAGAAA
AGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTGTAATCCCAGAGGCTGAGGCAGGCGGAT
CACCTGAGGTCGGGAGTTCGGGATCAGCCTGACCAACATGGAGAAACCCTACTGGAAATACAA
AGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTCCCAGCTGCTCAGGAGCCTGGCAACAAGAG
CAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

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FIGURE 364

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGRE
VAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDTYD
TDRDGRVGEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSDMATREELT
AFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPWVQTERQQFRDF
RDLNKDGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFVGSQAT
NYGEDLTRHHDEL

Important features:**Signal sequence:**

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302**N-myristoylation site.**

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

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FIGURE 363

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGCT
TCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGCCA
GGGGAGGGTGCACCAGGCGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAACTT
CCAGTACGACCATGAGGCTTTCCTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCACCCC
AGAGGAAAGCCAGGCCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGGACGGCGA
CGGCTGGGTGTCGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCACATACG
GGACTCGGTGAGCGCGGCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGGGTGGGA
GGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCCGGTGAAGAATTTTCATGACGTGGAGGA
TGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGGCGTTTCCGGGTGGCCGACCAGGA
TGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGGAGTTCCCTCA
CATGCGGGACATCGTGATTGCTGAAACCTGGAGGACCTGGACAGAAACAAAGATGGCTATGT
CCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGAGGAGCCGGCGTG
GGTGCAGACGGAGAGGCAGCAGTTCCGGGACTTCCGGGATCTGAACAAGGATGGGCACCTGGA
TGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCAGGACCAGCCCCCTGGTGGAAGCCAA
CCACCTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAAAGCGGAAATCCTGGG
TAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGGACCTGACCCGGCACCA
CGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCGCACAAATGACCGGAGGAG
GGGCCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCGCAGGAGGCAGATGCAGTCCCAGGC
ATCCTCCTGCCCCCTGGGCTCTCAGGGACCCCCTGGGTGGCTTCTGTCCCTGTACACCCCCA
ACCCAGGGAGGGGCTGTCATAGTCCCAGAGGATAAGCAATACCTATTTCTGACTGAGTCTCC
CAGCCCAGACCCAGGGACCCCTTGCCCCAAGCTCAGCTCTAAGAACCGCCCCAACCCCTCCAG
CTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCCTGGCCCCAGCCCTCTCCTGCCTG
GCCTGGCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAAAAGCCAGCGCCGGGACCTTGAAA
AA

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FIGURE 362

MRPLLVLALLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPG
EKGEGRPGPLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFD
RVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWPKPA
SLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

Important features:**Signal sequence.**

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

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FIGURE 361

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTG;
GGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAACT
GGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACTGCG
AGAGGACCCCGGCGTCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGCTGCT
CCTGGGCCTGGCGGCCGGCTCGCCCCCACTGGACGACAACAAGATCCCCAGCCTCTGCCCGGG
GCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGCCGCGATGG
CCGCGACGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGGCGAGGGGCGGGAGGCCGGG
ACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGGGCCACCGG
GCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTCCGAGAGCCG
GGTGCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACGAGCAGGGACA
TTACGACGCCGTACCCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTACTTGCCGTCCA
TGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGAATCATTGCCTC
TTTCTTCCAGTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGCGGCCATGGTGAG
GCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGC
CAGCATCAAGACAGACAGCACCTTCTCCGGATTTCTGGTGTACTCCGACTGGCACAGCTCCCC
AGTCTTTGCTTAGTGCCCCACTGCAAAGTGAGCTCATGCTCTCACTCCGAGAAGGAGGGTGTGA
GGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCTGGAATATTGTGAATGACTAGGGAGG
TGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATGGGAACAGTGGCTGTCTGCGATCA
GGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCAGTGGAGTGTGCTGTGCTGG
CAAGTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCACGGTGGGGTGTCTCTTCTGCTGCTC
CTCTGCTTCTCTGGATCCTCCCCACCCCTCCTGCTCCTGGGGCGGCCCTTTCTCAGAGAT
CACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 360

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSP TASDMLHMRWDEEL
AAFAKAYARQCVWGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQMC
GHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNIEPPGNVKGKRPYQEGTPCSQCPSG
YHCKNSLCEPIGSPEDAQDLPLYLVTEAPSF RATEASDSRKMGTPSSLATGIPAFLVTEVSGSL
ATKALPAVETQAPTSLATKDPSPMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKSTHVPI
PKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEAEELPPSSEVLASVFPAQD
KPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVVSGLN SGP
GHVWGPLLGLLLLPLVLGIF

Important features:**Signal sequence:**

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 339-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

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FIGURE 359

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTAC
TGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGTGG
AGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGAGAT
GGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGGCCACAACA
AGGAGCGCGGGCGCCGCGGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGTGCCGC
TGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCTGCAGCC
CAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATCGGCTGTG
GTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACTGGTGTGCA
ACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTCCGTGCTCCC
AATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGCCCGGAAGATG
CTCAGGATTTGCCTTACCTGGTAACCTGAGGCCCCATCCTTCCGGGCGACTGAAGCATCAGACT
CTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCTTGGTAACAGAGG
TCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCCCCAACTTCCTTAG
CAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCCTAACAACTGAGGTCCCTT
CCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTACCTTCCCCAAATCGA
CCCATGTTCCCTATCCCCAAATCAGCAGACAAAGTGACAGACAAAACAAAGTGCCCTCTAGGA
GCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAGGGAACTCCTACCCCATG
CCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTGAGGTCTTGGCCTCAGTTT
TTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGACCAACACGGGGCACACCTCCT
CCAAGTCCCTGCCCAATTTCCCCAATACCTCTGCCACCGCTAATGCCACGGGTGGGCGTGCCC
TGGCTCTGCAGTCGTCCTTGCCAGGTGCAGAGGGCCCTGACAAGCCTAGCGTTGTGTCAGGGC
TGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGACTACTGCTCCTGCCCTCCTCTGG
TGTTGGCTGGAATCTTCTTGAATGGGATACCACTCAAAGGGTGAAGAGGTCAGCTGTCCTCCTG
TCATCTTCCCCACCCTGTCCCCAGCCCCCTAAACAAGATACTTCTTGGTTAAGGCCCTCCGGAA
GGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCCATCCTGGAGGCACAAGGCCTGGCTG
GCTGCGAGCTCAGGAGGCCGCCTGAGGACTGCACACCGGGCCACACCTCTCCTGCCCCCTCCC
TCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCTCACTGCCTACCTGGCCTGGGGCTGTCT
GCCACACAGCATGTGCGCTCTCCCTGAGTGCCTGTGTAGCTGGGGATGGGGATTCTTAGGGG
CAGATGAAGGACAAGCCCCACTGGAGTGGGGTTCTTTGAGTGGGGGAGGCAGGGACGAGGGAA
GGAAAGTAACTCCTGACTCTCCAATAAAAACCTGTCCAACCTGTGAAA

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FIGURE 358

MVFPMTWLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVDPKNHVIVDCTDKHLTEIPGGI
PTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRCNCVPIPLGSKNNMCIKRLQIKPRSFSGL
TYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYRNPC
YVSYSIEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNLNQLQ
ILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWFKNINK
LQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSLKILRIR
GYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKISPSGDSSE
VGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQTLDSLKNS
IFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNRLDLLHSTAFEELHK
LEVLDISSNSHYFQSEGITHMLNFTKNLKVQLKMMNDNDISSSTSRTMESESLRTLEFRGNH
LDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSLAKNGLKSFSWK
KLQCLKNLETLDLSHNQLTTVPERLSNCSRLKNLILKNNQIRSLTKYFLQDAFQLRYLDLSS
NKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCAVWVFWVWNHTEVTIPYLATDVTCVGPGA
HKGQSVISLDLYTCELDLTNLILFSLISISVSLFLMVMMTASHLYFWDVWYIYHFCKAKIKGYQ
RLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLEERDWLPGQPVLENLSQ
SIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIIILIFLEKPFQKSKFLQLRKRLC
GSSVLEWPTNPFQAHYPFWQCLKNALATDNHVAYSQVFKETV

Important features:**Signal sequence:**

amino acids 1-26

Transmembrane domain:

amino acids 840-860

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FIGURE 357

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCCATTTTGGGAAGA
AGACTAAAAATGGTGTGTTTCCAATGTGGACACTGAAGAGACAAATTCTTATCCTTTTTAACATAATCCTAATTTCC
AAACTCCTTGGGGCTAGATGGTTTCTTAAACTCTGCCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG
ATCGTGGACTGCACAGACAAGCATTGTACAGAAATCTCTGGAGGTATTCCCACGAACACCACGAACCTCACCTC
ACCATTAACCACATACCAGACATCTCCCCAGCGTCCTTTACAGACTGGACCATCTGGTAGAGATCGATTTTCAGA
TGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAGC
TTTAGTGGACTCACTTATTTAAATCCCTTTACCTGGATGGAACAGCTACTAGAGATACCGCAGGGCCTCCCG
CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACAACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC
AACATAGAAATACTCTACCTGGGCCAAAACCTGTTATTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAA
GATGCCTTCCTAAACTTGACAAAGTTAAAGTGCTCTCCCTGAAAGATAACAATGTCACAGCCGTCCTACTGTT
TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATGATTTTAAATAAC
CTCAACCAATTACAAATCTTGACCTAAGTGGAATTGCCCTCGTTGTTATAATGCCCATTTCTTGTGCGCCG
TGTAATAATAATTCTCCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGACAGAATTAAAGTTTTACGTCTA
CACAGTAACTCTCTCAGCATGTGCCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAAGTGGATCTGTCC
CAAACTTCTTGGCCAAAGAAATTGGGGATGCTAAATTTCTGCATTTTCTCCCCAGCCTCATCCAATTGGATCTG
TCTTTCAATTTTGAACCTTCAGGTCTATCGTGCATCTATGAATCTATCACAAGCATTCTTCTCACTGAAAAGCCTG
AAAATTCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA
AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAGA
CTGAAAGTCATAGATCTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAT
GCCAGAACTTCTGTAGAAAGTTATGAACCCAGGTCTTGGAAACAATTACATTATTTTCAATATGATAAGTATGCA
AGGAGTTGCAGATTCAAAAACAAGAGGCTTCTTTCATGTCTGTTAATGAAAGCTGCTACAAGTATGGGCAGACC
TTGGATCTAAGTAAAAATAGTATATTTTTGTCAAGTCTCTGATTTTTCAGCATCTTCTTCTCAATGCCTG
AATCTGTGAGGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATTTCAACCTTTAGCAGAGCTGAGATATTTG
GACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCACAACTGGAAGTTCTGGAT
ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAACTTTACCAAGAACCTAAAGGTT
CTGCAGAACTGATGATGAACGACAATGACATCTCTTCCCTCCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA
ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAG
AATCTGCTAAAAATTAGAGGAATTAGACATCTCTAAAAATCCCTAAGTTTCTTGCCTTCTGGAGTTTTTGATGGT
ATGCCTCCAAATCTAAAGAATCTCTCTTTGGCCAAAAATGGGCTCAAATCTTTTCAAGTTGGAAGAACTCCAGTGT
CTAAAGAACCTGGAACTTTGGACCTCAGCCACAACCACTGACCACTGTCCCTGAGAGATTATCCAACCTGTTCC
AGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTTCTACAAGATGCCTTC
CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCCAGAAAATGTCTC
AACAATCTGAAGATGTTGCTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGG
GTTAACCATACGGAGGTGACTATTCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC
CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTCTCACTTTCCATA
TCTGTATCTCTTTTCTCATGGTGTGATGACAGCAAGTCACCTCTATTTCTGGGATGTGTGTTATTTACCAT
TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTAT
GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAGAGAGAAA
CATTTTAAATTTATGTCTCGAGGAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTTCCCAGAGCATA
CAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAGACTGAAAATTTTAAAGATAGCATTTTAC
TTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTTCAAG
TCCAAGTTCTCCAGCTCCGGAAAAGGCTCTGTGGGAGTTCTGTCTTGAAGTGGCCAACAACCCGCAAGCTCAC
CCATACTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA
ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCTGGC

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FIGURE 356

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGAIST
VRAGAE LRAVLALLRAGPGPGGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLESD
TLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGAASN
LSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPGRYLR
AGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATATSPVP
QRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITPSGSVIS
KFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMTVLGLVKLCFHESPSSQPRKESMGPP
GLES DPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Important features:**Signal sequence:**

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

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FIGURE 355

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTTCCTGACCCCAGAATAACTCAGGGCTGCACCGGGCCTG
GCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAAACTGTTGGCCGCTGGGCCCCGCGGGGGATTCTTGG
CAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGGAAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAG
GGCGGTGACCGCGCTCCAGACACAGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGC
GGGGCCTCAGAGAATGAGGCCGGCGTTGCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCGGGCGGCGG
CGAACACCCCCTGCGGACCGTGCTGGCTGCTCGGCCCTCGGGGGCCTGCTACAGCCTGCACCAGCTACCATGAA
GCGGCAGGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTCAGCACCGTGCGTGCGGGCGCCGAGCTGCG
CGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGGGCCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACT
GGAGCGCAGGCGTTCCCACTGCACCCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCGG
CGGTCTCGAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGCGGTACT
CCAGGCCACCGGTGGGGTCGAGCCCCGAGGCTGGAAGGAGATGCGATGCCACCTGCGCGCCAACGGCTACCTGTG
CAAGTACCAGTTTGAGGTCTTGTGTCTGCGCCGCGCCCCGGGGCCGCTCTAACTTGAGCTATCGCGCGCCCTT
CCAGCTGCACAGCGCCGCTCTGGACTTCAGTCCACCTGGGACCGAGGTGAGTGCGCTCTGCCGGGGACAGCTCCC
GATCTCAGTTACTTGCATCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTG
CCCCGGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGGCTTTGCCTG
CGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCAGTGGGGAAGGACAGCCGACCCT
TGGGGGGACCGGGGTGCCACCAGGCGCCCGCGGCCACTGCAACCAGCCCCGTGCCGCAGAGAACATGGCCAAT
CAGGGTCGACGAGAAGCTGGGAGAGACACCACTTGTCCCTGAACAAGACAATTAGTAACATCTATTCTGAGAT
TCCTCGATGGGGATCACAGAGCACGATGTCTACCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCAC
CCCATCAGGGAGCGTGATTTCCAAGTTTAAATCTACGACTTCCTCTGCCACTCCTCAGGCTTTTCTGACTCCTCCTC
TGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTTGGTGATCTTGACCATGACAGTACTGGGGCTTGT
CAAGCTCTGCTTTCACGAAAGCCCCTCTTCCAGCCAAGGAAGGAGTCTATGGGCCCCGCGGGCCTGGAGAGTGA
TCCTGAGCCCCGCTGCTTTGGGCTCCAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCT
GCGGGACAGAGCAGAGGGTGCCCTTGCTGGCGGAGTCCCCTCTTGGCTCTAGTGATGCATAGGGGAAACAGGGGACA
TGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACCTTACTTGTGTAACCTGACAA
TTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCACTGAGGAGCTAAATCAGAACTGCACACTCCTTC
CCTGATGATAGAGGAAGTGAAGTGCCTTTAGGATGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATT
TTCTTATGTTTATTCGGAGAATTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATAT
AATTTACATTAAAAAATAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTTCAGGCTAGGAGTATATTGG
TTCGAAATCCCAGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

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FIGURE 354

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFAPTQSQFYHL
FLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQTF
LGLDDLEYLQADFNLLRDIDPGAQDLNKLEVLILNDNLISTLPANVFQYVPITHLDLRGNRL
KTLPEYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENI PKNALIGRVVCEAPTRLQ GKDL
NETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKKTNGQEDHATPGSAPNGGTKIPGNW
QIKIRPTAAIATGSSRNKPLANS LPCPGGCSCDHIPGSG LKMNCNNRN VSSLADLKP KLSNVQ
ELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNYLDTLSRE
KFAGLQNLLEYLNVEYNAIQ LILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSLSKLSLHNN
YFMYLPVAGVLDQLTSIIQIDLHGNPWECSTIVPFKQWAERLGSEVLMSDLKCETPVNFFRK
DFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVLVPGLLLVFVT
SAFTVVGMLVFILNRKRKRSDANSSASEINSLQTVCDSSYWHNGPYNADGAHRVYDCGSHS
LSD

Important features:**Signal sequence:**

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697**N-myristoylation site:**amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

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FIGURE 353

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCTTTTCTTCTCCTTTCTGGCTTCGGACATTGG
AGCACTAAATGAACTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTGTTACTTTGTGATGAGATCGGGGATGA
ATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTTGCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTAC
AGGGGACGTTTGCAAAGAGAAGATCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAA
GGGCTTCACAAGTCTGCAGCGTTTCACTGCCCCGACTTCCCAGTTTTACCATTATTTCTGCATGGCAATTCCCT
CACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGGAAACAATGGCTTGCA
TGAAATCGTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGGCTGCACATCAACAACAACAAGATCAAGTC
TTTTCGAAAGCAGACTTTTCTGGGGCTGGACGATCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATAT
AGACCCGGGGGCTTCCAGGACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCCCTACC
TGCCAACGTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCCCTATGA
GGAGGTCTTGAGCAAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCCTGGGACTGCACCTGTGATCT
GCTCTCCCTGAAAGAATGGCTGGAAACATTCCCAAGAATGCCCTGATCGGCCGAGTGGTCTGCGAAGCCCCAC
CAGACTGCAGGGTAAAGACCTCAATGAAACCACCGAACAGGACTTGTGTCTTTGAAAAACCGAGTGGATTCTAG
TCTCCCGGCGCCCCCTGCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCA
AGAGGATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGATCAAAATCAG
ACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCTTAGCTAACAGTTTACCCTGCCCTGGGGGCTG
CAGCTGCGACCACATCCCAGGGTGGGTTTAAAGATGAACTGCAACAACAGGAACGTGAGCAGCTTGGCTGATTT
GAAGCCCAAGCTCTCTAACGTGCAGGAGCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTT
TGTGGATTACAAGAACCTCATTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACTTTCAA
GAACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGAGAAATTTCGCGGG
GCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCATCCTCCCGGGCACTTTCAATGCCAT
GCCAAACTGAGGATCCTCATTCTCAACAACAACCTGCTGAGGTCCCTGCCTGTGGACGTGTTGCTGGGGTCTC
GCTCTCTAAACTCAGCCTGCACAACAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAAGTTAACCTC
CATCATCCAGATAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCAGA
ACGCTTGGGTTCGGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTCTTTAGAAAGGATTTTAT
GCTCCTCTCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCTCGCCACGTTAACTTCGCACAGTAAAAA
CAGCACTGGGTGGCGGAGACCGGGACGCACTCCAACCTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTT
GGTCCCGGACTGCTGCTGGTGTGTTGTACCTCCGCCTTACCCTGGTGGGCATGCTCGTGTTTATCCTGAGGAA
CCGAAAGCGGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTGTGACTC
TTCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTGTGGCTCTCACTCGCTCTC
AGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCGATACATCCTTCCCCACCGCAGGCACCCCGGG
GGCTGGAGGGGGCTGTACCCAAATCCCCGCGCCATCAGCCTGGATGGGCATAAGTAGATAAATAACTGTGAGCTC
GCACAACCGAAAGGGCCTGACCCCTTACTTAGCTCCCTCCTTGAACAAGAGCAGACTGTGGAGAGCTGGGAGA
GCGCAGCCAGCTCGCTCTTTGCTGAGAGCCCCCTTTGACAGAAAGCCAGCACGACCCTGCTGGAAGAACTGACA
GTGCCCTCGCCCTCGCCCCGGGGCCTGTGGGGTTGGATGCCGCGGTTCTATACATATATACATATATCCACATC
TATATAGAGAGATAGATATCTATTTTTCCCTGTGGATTAGCCCCGTGATGGCTCCCTGTTGGCTACGCAGGGAT
GGGCAGTTGCACGAAGGCATGAATGTATTGTAAATAAGTAACTTTGACTTCTGAC

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FIGURE 352

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLLDCSRKRLARLPEPLPSW
VARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSPANITLLSLAGNRIVEILPEHLKEFQSLETL
DLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEPGYFDNLANTLLVLKLNRRNRISAIPPKMFKLPLQHLLELNRN
KIKNVDGLTFQGLGALKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNITEITKGWLYGLLMLQELHLSQNAIN
RISPDWEFCQKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNESWTI
EDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMKKLOQLHLNTSSLLCDC
QLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASS
SDSPMTFAWKKDNELLHDAEMENYAHLRAQGGVEYTTILRLREVEFASEGKYQCVISNHFSSYSVKAKLTVN
MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDGSTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYS
CTAONSAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTERHFFAAGNQ
LLIIVDSVDSDAGKYTCMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDGWATVGVVIAVCCVVGTSIV
WVVIYYHTRRRNEDCSITNTDETNPADIPSYLSSQGTADLRQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGT
CHIDNSSEADVEAATDLFLCPFLGSTGPMYLGKNVYGSDFETYHTGCSPPDPTVLMDDHYEPSYIKKKECYPCSH
PSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDIFSANPEPASVASSNSFMGTFGKALRRPHL
DAYSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQENHICTFKQTLNRYRTPNFQSYDLDT

Important features:**Signal sequence:**

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020**Glycosaminoglycan attachment site.**

amino acids 886-890

Casein kinase II phosphorylation site.amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085**Tyrosine kinase phosphorylation site.**

amino acids 667-675

N-myristoylation site.amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939**Leucine zipper pattern.**

amino acids 58-80, 65-87

FIGURE 351

BNSDOCID: <WO_0140466A2_1_>

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FIGURE 350

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIPE
GVTVLYLHNNQINNAGFP AELHNVQSVHTVYLYGNQLDEFEMNLPKNVRVLHLQENNIQTISR
AALAQLLKLEELHLDNNSISTVGVEDGAFREAI SLKLLFLSNHLSSVPVGLPVDLQELRVDE
NRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPDLPGT
HLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNNPWFCD
CSIKWVTEWLKYIPSSLNVRGFMCGQPEQVRGMVRELNMNLLSCPTTTPGLPLFTPAPSTAS
PTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWGGRERVTPPISERIQLSIHVNDTSIQVSW
LSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPSTYRICLVPLDAFN YRAV
EDTICSEATTHASYLNNGSNTASSHEQTTSMSGSPFLLAGLIGCAVIFVLVLLSVFCWHMH
KKGRYTSQKWKNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNDQLLKGD FRLQPIYTP
NGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Important features:**Signal peptide:**

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639**Amidation site.**

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

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FIGURE 349

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAGGACAGCAGCAAAG
AGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTACCATACGCCCTCAGGACGTTCCCTCTA
GCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGTCATTTTGATTTTGCTGTTTATTTTTTTTTTCTTTTTCTT
TTTCCACACATTGTATTTTATTTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCCAGCCATGGGG
CTTTTTTCTGAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCCCTA
GTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTGCCTCTTGGGATCCCGG
AGGGCGTAACCGTACTCTACCTCCACAACAACCAATTAATAATGCTGGATTTCCTGCAGAACTGCACAATGTAC
AGTCGGTGCACACGGTCTACCTGTATGGCAACCAACTGGACGAATTCCTCATGAACCTTCCCAAGAATGTCAGAG
TTCTCCATTTGCAGGAAAACAATATTCAGACCATTTACGGGCTGCTCTTGCCCAGCTCTTGAAGCTTGAAGAGC
TGCACCTGGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCCTCAAAT
TGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCCTGTGGACTTGCAAGAGCTGAGAGTGG
ATGAAAATCGAATTGCTGTCTATATCCGACATGGCCTTCAGAATCTCACGAGCTTGGAGCGTCTTATTGTGGACG
GGAACCTCCTGACCAACAAGGTATCGCCGAGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTG
TACGTAATTGCTGTCCACCCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACC
AGATAAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCAACAACCAAC
TGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTCACTGCTCGGAATAACCCCTTGGT
TTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAAATATATCCCTTCATCTCTCAACGTGCGGGGTTTCA
TGTGCCAAGGTCTGAACAAGTCCGGGGGATGGCCGTGAGGAATTAAATATGAATCTTTTGTCTGTCCCACCA
CGACCCCGGCCTGCCTCTCTTCACCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCCTCTCTA
TTCCAAACCCTAGCAGAAGCTACACGCCTCCAACCTCCTACCACATCGAAACTTCCCACGATTCTGACTGGGATG
GCAGAGAAAGAGTGACCCCACTATTTCTGAACGGATCCAGCTCTCTATCCATTTTGTGAATGATACTTCCATTC
AAGTCAGCTGGCTCTCTCTCTTACCGTGATGGCATACAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAG
GGGGCATCGTTCAGGAGCGCATAGTCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCA
CCTATCGGATTTGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTGTTTCAAGAGGCCA
CCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGACGTCCACAGCATGG
GCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTTGTGCTGGTGGTCTTGCTCAGCGTCTTTT
GCTGGCATATGCACAAAAAGGGGCGCTACACCTCCCAGAAGTGGAATACAACCGGGGCGCGGGAAGATGATT
ATTGCGAGGCAGGCACCAAGAAGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTTTCAATCGTCTCCTTAA
ATAACGATCAACTCCTTAAAGGAGATTTTCACTGCAGCCATTTACACCCCAAATGGGGGCATTAATTACACAG
ACTGCCATATCCCCAACAACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGCACTGCCATACGTGACAGC
CAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAACACACTCGTGTGTGCACATAAAGACACGCAG
ATTACATTTGATAAATGTTACACAGATGCATTTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAA
TGGGATTTAAAAAAGTGCTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTTGTAACTCTTTGCTTTTTTAA
TCTT

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FIGURE 348

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDET VVAGGTVVLKCQVKDHEDSSLQWS
NPAQQTLYFGEKRALRDNRIQLVTSTPHELSSISINVALADEGEYTCSIFTMPVRTAKSLVTV
LGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFT
VSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQKLLL
HCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLN
VNDPSPVPSSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTAEAKGSDDAPDADT
AIINAEGGQSGGDDKKEYFI

Important features:**Signal sequence:**

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

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FIGURE 347

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAACA
TCGTAGTCCACCCCCTCCCCATCCCCAGCCCCGGGGATTCAAGGCTCGCCAGCGCCCAGCCAG
GGAGCCGGCCGGGAAGCGCGATGGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGCTGT
TCGCCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGGACAT
CTGATGAAACAGTGGTGGCTGGTGGCACCCTGGTGCTCAAGTGCCAAGTGAAAGATCACGAGG
ACTCATCCCTGCAATGGTCTAACCCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGAGAGCCC
TTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGCATCAGCA
ATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGTGCGAACTG
CCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTTATAAATCTT
CATTACGGGAAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAGCCTGCAGCCC
GGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCATACAGGAAGATC
CCAATGGTAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCCGGGAGGATGATG
GGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGACAGATCCACCTCTC
AACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCCTCCCCATCCTCGTG
AGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCCCCCAGCAGTACCTAT
GGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGTGCCCTGATCTTCCCTT
TCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAGCAACATGGGCAGCTACA
AGGCCTACTACACCCTCAATGTTAATGACCCCAGTCCGGTGCCCTCCTCCTCCAGCACCTACC
ACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGCTGCTCATCATGCTCATCTTCC
TTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACATGAGGCAAAGGCTCCGACG
ATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCGGGCAGTCAGGAGGGGACGACA
AGAAGGAATATTTTCATCTAGAGGCGCCTGCCCCACTTCCTGCGCCCCCAGGGGCCCTGTGGGG
ACTGCTGGGGCCGTCACCAACCCGGACTTGTACAGAGCAACCGCAGGGCCGCCCTCCCGCTT
GCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGCTTTGGGTGCGGTTTTGTACTCGGT
TTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGGTGCCCTCAGCCCTTCCGTGGCTT
CTCTGCATTTGGGTTATTATTATTTTTGTAACAATCCCAAATCAAATCTGTCTCCAGGCTGGA
GAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACAAACAAAAACA

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FIGURE 346

MGSRCALALAVLSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGAGPPPCACRTFFRVC
LKHYQASVSPEPPCTYGS AVTPVLGVDSFSLPDGGGADSAFSNPIRFFPGFTWPGTFSLIIEA
LHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKYSYRFVCD EHY YGEGCS
VFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLP GCDEQHGFCDKPGECKCRVGWQGR
YCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPKNGATCTNTGQGSYTCS
CRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCTCPPGFYGKICELSAMTCADGPCFNG
GRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQAGFSGRHCD
DNVDDCASSPCANGGTCRDGVNDFSCCTPPGYTGRNCSAPVSRCEHAPCHNGATCHERGHRYV
CECARGYGGPNCQFLLPELPPGPAVVDLTEKLEGQGGPFPWVAVCAGVILVLM LLLGCAAVV
CVRLRLQKHRPPADPCRGETETMNNLANCQREKDISVSIIGATQIKNTNKKADFHGDHSADKN
GFKARYPAVDYNLVQDLKGDDTAVRDAH SKRDTKCQPQGS SGEKGTPTTLRGGEASERKRPD
SGCSTSKDTKYQSVYVISEEKDECVIATEV

Important features:**Signal sequence:**

Amino acids 1-21

Transmembrane domain:

Amino acids 546-566

N-glycosylation site:

Amino acids 477-481

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 660-664

Tyrosine kinase phosphorylation sites:

Amino acids 176-185;252-261

N-myristoylation sites:Amino acids 2-8;37-43;40-46;98-104;99-105;262-268;281-287;
282-288;301-307;310-316;328-334;340-344;378-384;387-393;512-518;
676-682;683-689;695-701**Aspartic acid and asparagine hydroxylation sites:**

Amino acids 343-355;420-432;458-470

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 552-563

EGF-like domain cysteine pattern signature:Amino acids 243-255;274-286;314-326;352-364;391-403;429-441;
467-479;505-517

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FIGURE 343

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCCCTTTTCATTGACAACTGACTTTTTTTTATTTCT
TTTTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT
CTGTGTTTTGGGGTTTTCTTCTCCCTCCCCTGACATTGGCATTGCTTAGTGTTGTGTGGGGAGGGAGACCACGTGG
GCTCAGTGCTTGGCTTGCACCTTATCTGCCTAGGTACATCGAAGCTCTTTGACCTCCATACAGTGATTATGCCTGTC
ATCGCTGGTGGTATCCTGGCGGCCTTGCTCCTGCTGATAGTTGTCTGCTCTGTCTTTACTTCAAAATACACAAC
GCGCTAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAAACCAGACAAGGTGTGGTGGGCCAAG
AACAGCCAGGCCAAAACCATTGCCACGGAGTCTTGCTCCTGCCCTGCAGTGCTGTGAAGGATATAGAATGTGTGCC
AGTTTTGATTCCCTGCCACCTTGCTGTTGCGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAAA
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAG
CTCCCCATCAGTTTTCATGGAAAATAACTCAGTGCCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGGCAACCCTTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGGAATGCTGATAAACCCAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGGAAGTACGTTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGTGGTCTTAAAGGCTGCCAGCGCCTTGCCAAAATGGAGCTTGTA
AGAAGGCTCATGCCATTGACCCTCTTAATTCTCTCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAGCATCAGAATTATCTTTTCCCTATGTCCAGCTT
GATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAAGTCTTTGACGGAACCTCCAGCAATGGGCCCTCTGCTAGGG
CAAGTCTGCAGTAAAAACGACTATGTTCCCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCCTAACATCTCTATTCCAACTGT
GGCGGTTACCTGGATACCTTGAAGGATCCCTTACCAGCCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT
TGTGTGTGGCACATAAAGTGGAGAAAGATTACAAGATAAACTAACTTCAAAGAGATTTTCTAGAAATAGAC
AAACAGTGCAAATTTGATTTTCTTGCCATCTATGATGGCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT
GGCCGTGTGACTCCCACCTTCGAATCGTCATCAAACCTCTCTGACTGTCTGTGTTGTCTACAGATTATGCCAATTCT
TACCGGGGATTTTCTGCTTCTTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCAACTAAAA
GACCCAACCTTGACAGACCAAAATTATCAAAATGTTGTGGAATTTTCTGTCCCTCTTAATGGATGTGGTACAATCAGA
AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACC
CGTCAGAAACAACTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA
GAAGATGATGTAATACAAAGTCAAAATGCACTGGGCAAATATAACACCAGCATGGCTCTTTTGAATCCAATTCA
TTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTTGAACCAAACTCTTTTGTTCAGTTAGTCTGCAC
ACCTCAGATCCAAATTTGGTGGTGTCTTGATACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTCCGAGATGAACTTGTAAAGGTGTATCCCTTATTTGGACACTATGGGAGA
TTCCAGTTAATGCCTTTAAATTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAAGTTTTGATATGTGAT
AGCAGTGACCACCAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCATATAAATGG
AAAACAGATTCCATCATAGGACCCATTCTGCTGAAAAGGGATCGAAGTGCAAGTGGCAATTCAGGATTTTCAGCAT
GAAACACATGCGGAAGAACTCCAAACCAGCCTTTCAACAGTGTGCATCTGTTTTCTTTCATGGTTCTAGCTCTG
AATGTGGTGAATGTAGCGACAATCACAGTGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTG
CAGAATATTAACAGGTCCAACCCCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAAAA

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FIGURE 342

MLRFLPDLAFSFLLILALGQAVQFQEYVFLQFLGLDKAPSPQKFQVPYILKKIFQDREAAAT
TGVSRDLCYVKELGVRGNVLRFLPDQGGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQ
LGLDLGPNSYYNLGPELELALFLVQEPHVWGQTPKPGKMFVLRSPWPQGAVHFNLLDVAKD
WNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTLNPDQCHPSRKRRAA
IPVPLKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYPCHGECPPSLTISLNSSNYAFMQA
LMHAVDPEIPQAVCIPTKLSPISMLYQDNNDNVILRHYEDMVVDECGCG

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 112-116, 306-310

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 96-100

N-myristoylation site.

amino acids 77-83

TGF-beta family proteins.

amino acids 264-299, 327-341, 345-364

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FIGURE 341

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAGG
CCATGCTTCGTTTCTTGCCAGATTTGGCTTTCAGCTTCCTGTAAATTCTGGCTTTGGGCCAGG
CAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCACCCC
AGAAGTTCCAACCTGTGCCTTATATCTTGAAGAAAATTTTCCAGGATCGCGAGGCAGCAGCGA
CCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGGAATGTACTTC
GCTTTCTCCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCTCCTGCC
TGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACATTGGCCC
AGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGAAGTGGCTC
TGTTCTGTTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTAAAATGTTTG
TGTTGCGGTCAGTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGATGTAGCTAAGG
ATTGGAATGACAACCCCCGGAAAAATTTTCGGGTTATTCCTGGAGATACTGGTCAAAGAAGATA
GAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGATGCTCCCTTCATG
CTTCCCTGCTGGTGGTGACTCTCAACCCTGATCAGTGCCACCCTTCTCGGAAAAGGAGAGCAG
CCATCCCTGTCCCCAAGCTTTCTTGTAAGAACCTCTGCCACCGTCACCAGCTATTCATTAAGT
TCCGGGACCTGGGTTGGCACAAGTGGATCATTGCCCCCAAGGGGTTTCATGGCAAATTAAGTCC
ATGGAGAGTGTCCCTTCTCACTGACCATCTCTCTCAACAGCTCCAATTATGCTTTTCATGCAAG
CCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTGTATCCCCACCAAGCTGTCTC
CCATTTCCATGCTCTACCAGGACAATAATGACAATGTCATTCTACGACATTATGAAGACATGG
TAGTCGATGAATGTGGGTGTGGGTAGGATGTCAGAAATGGGAATAGAAGGAGTGTTCTTAGGG
TAAATCTTTTAATAAAACTACCTATCTGGTTTATGACCACTTAGATCGAAATGTC

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FIGURE 340

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQDEVPPQQTVAPOQQR
RSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSGQTNKSSCTTTRDTVCQCEKGSFQDKN
SPEMCRTCRTGCPGMVKVSNCTPRSDIKCKNESAASSTGKTPAAEETVTTILGMLASPYHYLIIVVLVIILAV
VVVGFSRKKFISYLGICSGGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQGQEL
AELTGVTVESPEEPQRLLEQAEAGCQRRRLLPVNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKLFYE
EDEAGSATSCL

Important features:**Transmembrane domains:**

amino acids 35-52, 208-230

N-glycosylation sites.

amino acids 127-131, 182-186, 277-281

Glycosaminoglycan attachment site.

amino acids 245-249

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 260-264

N-myristoylation sites.

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276, 297-303, 380-386

ATP/GTP-binding site motif A (P-loop).

amino acids 185-193

TNFR/NGFR cysteine-rich region.

amino acids 99-139

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FIGURE 339

GCGAGAACCTTTGCACGCGCACAACTACGGGGACGATTTCTGATTGATTTTGGCGCTTTCGATCCACCCTCCT
CCCTTCTCATGGGACTTTGGGGACAAAGCGTCCCGACCGCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGCCA
GGACAGCGTCGGGAACCAGACCATGGCTCCTGGACCCCAAGATCCTTAAGTTCGTCGCTTTCATCGTCGCGGTTT
TGCTGCCGTTCCGGTTGACTCTGCCACCATCCCCGGCAGGACGAAGTTCCCCAGCAGACAGTGGCCCCACAGC
AACAGAGGCGCAGCCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAATATACTGGAGCCTGTAACC
CGTGACAGAGGGTGTGGATTACACCATTGCTTCCAACAATTTGCCTTCTGCCTGCTATGTACAGTTTGTAAAT
CAGGTCAAACAAATAAAAGTTCTGTACCACGACCAGAGACACCGTGTGTGAGTGTGAAAAAGGAAGCTTCCAGG
ATAAAAACTCCCCTGAGATGTGCCGGACGTGTAGAACAGGGTGTCCCAGAGGGATGGTCAAGGTGAGTAATTGTA
CGCCCCGGAGTGACATCAAGTGCAAAAATGAATCAGCTGCCAGTTCCACTGGGAAAACCCAGCAGCGGAGGAGA
CAGTGACCACCATCCTGGGGATGCTTGCCTCTCCCTATCACTACCTTATCATCATAGTGGTTTTAGTCATCATTT
TAGCTGTGGTTGTGGTTGGCTTTTCATGTGCGGAAGAAATTCATTTCTTACCTCAAAGGCATCTGCTCAGGTGGTG
GAGGAGGTCCCGAACGTGTGCACAGAGTCTTTTCCGGCGGCGTTTCATGTCTTCACGAGTTCCTGGGGCGGAGG
ACAATGCCCGCAACGAGACCCCTGAGTAACAGATACTTGCAGCCACCCAGGTCTCTGAGCAGGAAATCCAAGGTC
AGGAGCTGGCAGAGCTAACAGGTGTGACTGTAGAGTGCAGAGGAGCCACAGCGTCTGCTGGAACAGGCAGAAG
CTGAAGGGTGTGAGAGGAGGAGGTGCTGGTTCCAGTGAATGACGCTGACTCCGCTGACATCAGCACCTTGCTGG
ATGCTCCGCAACACTGGAAGAAGGACATGCAAAGGAAACAATTCAGGACCAACTGGTGGGCTCCGAAAAGCTCT
TTTATGAAGAAGATGAGGCAGGCTCTGCTACGTCCTGCCTGTGAAAGAATCTCTTCAGGAAACAGAGCTTCCCT
CATTTACCTTTTCTCTACAAAGGGAAGCAGCCTGGAAGAAACAGTCCAGTACTTGACCCATGCCCCAACAACT
CTACTATCCAATATGGGGCAGCTTACCAATGGTCTTAGAATTTGTAAACGCACTGGAGTAATTTTTATGAAAT
ACTGCGTGTGATAAGCAAACGGGAGAAATTTATATCAGATTCTTGGCTGCATAGTTATACGATTGTGTATTAAGG
GTCGTTTTAGGCCACATGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGATAGGCTGAGGCAGGTGGATTGCTT
GAGCTCGGGAGTTTGAGACCAGCCTCATCAACACAGTGAAACTCCATCTCAATTTAAAAAGAAAAAAGTGGTTT
TAGGATGTCATTTCTTGCAGTTCTTCATCATGAGACAAGTCTTTTTTCTGCTTCTTATATTGCAAGCTCCATCT
CTACTGGTGTGTGCATTTAATGACATCTAACTACAGATGCCGCACAGCCACAATGCTTTGCCTTATAGTTTTTTA
ACTTTAGAACGGGATTATCTTGTTATTACCTGTATTTTTCAGTTTTCGGATATTTTGACTTAATGATGAGATTATC
AAGACGTAGCCCTATGCTAAGTCATGAGCATATGGACTTACGAGGGTTCGACTTAGAGTTTTGAGCTTTAAGATA
GGATTATTGGGGCTTACCCCCACCTTAATTAGAGAAACATTTATATTGCTTACTACTGTAGGCTGTACATCTCTT
TTCCGATTTTTGTAAATGATGTAAACATGAAAAACTTTAGGAAATGCACTTATTAGGCTGTTTACATGGGTTG
CCTGGATACAAATCAGCAGTCAAAAATGACTAAAAATATAACTAGTGACGGAGGGAGAAATCCTCCCTCTGTGGG
AGGCACTTACTGCATTCCAGTTCTCCCTCCTGCGCCCTGAGACTGGACCAGGGTTTGATGGCTGGCAGCTTCTCA
AGGGGCAGCTTGTCTTACTTGTTAATTTTAGAGGTATATAGCCATATTTATTTATAAATAAATATTTATTTATTT
ATTTATAAGTAGATGTTTACATATGCCCAGGATTTTGAAGAGCCTGGTATCTTTGGGAAGCCATGTGTCTGGTTT
GTCGTGCTGGGACAGTCATGGGACTGCATCTTCCGACTTGTCCACAGCAGATGAGGACAGTGAGAATTAAGTTAG
ATCCGAGACTGCCAAGAGCTTCTCTTCAAGCGCCATTACAGTTGAACGTTAGTGAATCTTGAGCCTCATTGGG
CTCAGGGCAGAGCAGGTGTTTATCTGCCCGGCATCTGCCATGGCATCAAGAGGGAAGAGTGACGGTGTCTGGG
AATGGTGTGAAATGGTTGCCGACTCAGGCATGGATGGGCCCTCTCGCTTCTGGTGGTCTGTGAACTGAGTCCCT
GGGATGCCTTTTAGGGCAGAGATTCTGAGCTGCGTTTTAGGGTACAGATTCCCTGTTTGAGGAGCTTGGCCCCCT
CTGTAAGCATCTGACTCATCTCAGAGATATCAATTCCTAAACACTGTGACAACGGGATCTAAAATGGCTGACACA
TTTGTCTTGTGTACGTTCCATTATTTTATTTAAAAACCTCAGTAATCGTTTTAGCTTCTTTCCAGCAAACCTCT
TCTCCACAGTAGCCAGTCGTGGTAGGATAAATTACGGATATAGTCATTCTAGGGGTTTACGCTTTTCCATCTC
AAGGCATTGTGTGTTTTGTTCCGGGACTGGTTTGGCTGGGACAAAGTTAGAAGTGCCTGAAGTTCGCACATTGAG
ATTGTTGTGTCCATGGAGTTTTAGGAGGGGATGGCCTTTCCGGTCTTCGCACTTCCATCCTCTCCCACTTCCATC
TGGCGTCCACACCTTGTCCCTGCACTTCTGGATGACACAGGGTGTGCTGCCTCCTAGTCTTTGCCTTTGCTG
GGCCTTCTGTGACAGGAGACTTGGTCTCAAAGCTCAGAGAGAGCCAGTCCGGTCCCAGCTCCTTTGTCCTTCTCTC
AGAGGCCCTTCTTGAAGATGCATCTAGACTACCAGCCTTATCAGTGTTAAGCTTATTCCTTTAACAATAAGCTTC
CTGACAACATGAAATTGTTGGGGTTTTTTGGCGTTGGTTGATTTGTTTAGGTTTTGCTTTATACCCGGGCCAAAT
AGCACATAACACCTGGTTATATATGAAATACTCATATGTTTATGACCAAATAAATATGAAACCTCATRTTAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 338

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHG EVSSS
QPWEVPMFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMP SRNLSLRLEGLQEKDSGPYSC
SVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQWDR
QLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGA AVVAG
AVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTL PWP KCSSDTISKNGTLSSVTS
ARALRPPHGP RP RGALTPTPSLSSQALPSPRLPTTDGAHPQPISP I PGGVSSSGLSRMGAVPV
MVPAQSQAGSLV

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

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FIGURE 440

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEVK
HCTDQISFKKRLSLKKSWWK

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FIGURE 441

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGATG
GGGTTGCTGGTTTAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCACC
ACCTCCGCCAGGAAGTGCAGGCCCCACCTGTCTGCAACCCAGCTGAGGCC**ATG**CCCTCCCCAGG
GACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCTCCAG
CTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAA
GCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCCGGAAGATGGAGGTCAAGCAGAAGGGGC
AGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGTCAGGGGT
TCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGGGAAGAGGC
CAAAGAGGCCCCAGCCGACAAG**TGA**TCGCCCACAAGCCTTACTCACCTCTCTCTAAGTTTAGA
AGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTACAAGCTCAGG
AGGCGAATAAATGTTCAAACCTGTA

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FIGURE 442

MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDGG
QAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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FIGURE 443

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTCG
TGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGTTT
CTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTGCTC
CTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCTGAGT
ATGTCCCCCACCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATCTTACA
CCTCTACTTGAGTATGTCCCTAACCCTGAGCCCCCACGCCTGGGGCCAGAGTCTTTGTCCCC
CGTGTGCGCATGTGTTTCAAGGTGAGCCTCTCCAGAAAGTGAGATCATGGACAAAAGGGCAAA
TCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAACTCACGCCG
AGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAAATGTTTCAAGACAAATGGA
ATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTTCCAAAACAC
AAGTAGAAATTTCTAACAATGAAATATATTACAGGCAGGTACCCACTAACCACAACTGAAG
CGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTGAGTCATGTTGCT
GAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGTAACAACAACCTCC
CTGCTCCTGGCACCAGCCGTTTTGGTTCATGGTGGGCCAGCTGCAAAGCGTCTTCCATTCTCTG
GGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGTTTCTGTGGACACGGGCAGCAGAGTG
TGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCAACCCCTGGTCAGGGCA
GAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGAGCATCCCCTGCCTGCAG
TTGTGGCAAGAACGCCCAGCTCAGAATGAACACACCCACCAAGAGCCTCCTTGTTTATAACC
ACAGGTTACCCTACAAACCACTGTCCCCACACAACCCTGGGGATGTTTTAAACACACACCTC
TAACGCATATCTTACAGTCACTGTTGTCTTGCCTGAGGGTTGAATTTTTTTTAAATGAAAGTGC
AATGAAAATCACTGGATTAAATCCTACGGACACAGAGCTGAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAA

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FIGURE 444

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDLGLVHLGQLLIFHIYLSMSPTLSPRSPQGWV
VRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQAQ
QEAELTPRPAGVVPGA

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FIGURE 445

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGA**ATG**GACTGGCCTCACAACCTGC
TGTTTCTTCTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAAGA
GGAAGGGGCAAGGGCGGCCTGGGCCCCCTGGCCCCTGGCCCTCACCAGGTGCCACTGGACCTGG
TGTCACGGATGAAACCGTATGCCCCGATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGG
CCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTGCAGCTGTGGA
TGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCCGTATCC
CCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACCATGCAGG
AGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCCCTGTGCGCCGCCGCCTCTGCC
CGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCGCTGTGGGCT
GCACCTGCATCTTCT**TGA**ATCACCTGGCCCAGAAGCCAGGCCAGCAGCCGAGACCATCCTCCT
TGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAAGCAAG

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FIGURE 446

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEYE
RNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRI PVDLPEARCLCLGC
VNPFTMQEDRSMVSPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

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FIGURE 447

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAGA
TGGAGCTCTCGAAGGCCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCTAT
CACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGGTGC
CCAAGCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTGGATG
GAGATACCAACACATCCACCCAGGAGGTGGTACAATACTGAGGAGACTGGGGATGACCGGT
TCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAGAACCAG
GGGAGAGGTGCCGAAGTTTCATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAAGGACTAC
TGGAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTTGGAGGGAAGCGGTTGA
TGGAGAAGGCTTCCCTCCCCTCCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTATGGTTATCC
CTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCTACTAACAGAC
TTGCTACTCACTGGGAACCCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTGCTGTTTCCTCT
GTCCTGTCAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAAGTCTTCCAAGCGACT
GTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAAATTATGGCTGGGCCTTCTACATG
GCCTGGCTCTCCTTACCTGCTGCATGGCGTCGGCTGTCACCACCTTCAACACGTACACCAGG
ATGGTGCTGGAGTTCAAGTGCAAGCATAGTAAGAGCTTCAAGGAAAACCCGAAGTGCCTACCA
CATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCACCGTGGGTCTTTGACC
AGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGGGAGTCGACTTCTACTCC
GAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTGAAAGAAGCAGTTAGGTCA
TCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGAGTAGGCTTGAGCCCTACCT
TACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCGTCTCTTGAGCATGGTTTTTA
GAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTCCTAAGGGATTCTTGGGTGCCA
CTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTCACCCACCCACATCTCACACATCCAGAA
TTCCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGCTAAACCATGGAGATAAAAAGAAG
AGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

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FIGURE 448

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMPV
SLDGD TNTSTQEVVQYNWETGDDRFSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKRGE
KGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPLGLCGKNPMVIPGNADHLHRTSIHQLP
TNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSCQLGSRRLTTCLELWLG
LLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

FIGURE 449

BNSDOCID: <WO_ 0140466A2 : >

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FIGURE 450

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPHN
LSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQIT
QLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRI FQDCRSLKF
LDIGYNQLKSLARNSFAGL FKLTELHLEHNDLVKVNFAHFPR LISLHSLCLRRNKVAIVVSSL
DWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDNRLTYIEPRIILNSWKSLSITLAGNL
WDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDAVYAFHLCEDGA EPTSGHLLSAV
TNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMALIFSFLI
VVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNHIEGALVII
NEYGSCTCHQQPARECEV

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FIGURE 451

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGGCGTTCTCCAGTCACCCTCCCGCCGTTAC
CCGCGGCGCGCCCGAGGGAGTCTCCTCCAGACCCTCCCTCCCGTTGCTCCAAACTAATACGGA
CTGAACGGATCGCTGCGAGGGTGGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCAACT
ACCATCCATAGCCAGATAGATTATCTTACACTGAACTGATCAAGTACTTTGAAAATGACTTTCG
AAATTTATCTTGGTGTCTTTCATACTTGCTGCACTGAGTCTTTCAACCACCTTTTCTCTCCAA
CTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGATGGATTCCGTTGGGATTACTTATATAAA
GTTCCAACGCCCCATTTTCATTATATTATGAAATATGGTGTTCACGTGAAGCAAGTTACTAAT
GTTTTTATTACAAAAACCTACCCTAACCATTATACTTTGGTAACTGGCCTCTTTGCAGAGAAT
CATGGGATTGTTGCAAATGATATGTTTGATCCTATTTCGGAACAAATCTTTCTCCTTGGATCAC
ATGAATATTTATGATTCCAAGTTTTGGGAAGAAGCGACACCAATATGGATCACAACCAGAGG
GCAGGACATACTAGTGGTGCAGCCATGTGGCCCGGAACAGATGTAAAAATACATAAGCGCTTT
CCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAGAGTTGCCAAAATTGTT
GAATGGTTTACGTCAAAAGAGCCCATAAATCTTGGTCTTCTCTATTGGGAAGACCCTGATGAC
ATGGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCCTGTCATTTTCAGATATTGACAAG
AAGTTAGGATATCTCATACAAATGCTGAAAAAGGCAAAGTTGTGGAACACTCTGAACCTAATC
ATCACAAGTGATCATGGAATGACGCAAGTCTCTGAGGAAAGGTTAATAGAAGTTGACCAGTAC
CTGGATAAAGACCACTATAACCCTGATTGATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAA
GGTAAATTTGATGAAGTCTATGAAGCACTAACTCACGCTCATCCTAATCTTACTGTTTACAAA
AAAGAAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTCAACCAATCATAGCA
GTGGCTGATGAAGGGTGGCACATTTTACAGAATAAGTCAGATGACTTTCTGTTAGGCAACCAC
GGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTTAGCCCATGGTCTGCCTTCAGA
AAGAATTTCTCAAAAGAAGCCATGAACTCCACAGATTTGTACCCACTACTATGCCACCTCCTC
AATATCACTGCCATGCCACACAATGGATCATTCTGGAATGTCCAGGATCTGCTCAATTCAGCA
ATGCCAAGGGTGGTCCCTTATACACAGAGTACTATACTCCTCCCTGGTAGTGTTAAACCAGCA
GAATATGACCAAGAGGGGTACATACCCTTATTTTCATAGGGGTCTCTCTTGGCAGCATTATAGTG
ATTGTATTTTTTTGTAATTTTCATTAAGCATTTAATTCACAGTCAAATACCTGCCTTACAAGAT
ATGCATGCTGAAATAGCTCAACCATTATTACAAGCCTAATGTTACTTTGAAGTGGATTGTCAT
ATTGAAGTGGAGATTCCATAATTATGTCAGTGTTTAAAGGTTTCAAATTCTGGGAAACCAGTT
CCAAACATCTGCAGAAACCATTAAAGCAGTTACATATTTAGGTATACACACACACACACACA
CACATACACACACACGGACCAAAATACTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGT
CTCCATTGTTCACTGTAGCATAGGGATAGATAAGATCCTGCTTTATTTGGACTTGGCGCAGAT
AATGTATATATTTAGCAACTTTGCACTATGTAAAGTACCTTATATATTGCACTTTAAATTTCT
CTCCTGATGGGTACTTTAATTTGAAATGCACTTTATGGACAGTTATGTCTTATAACTTGATTG
AAAATGACAACTTTTTGCACCCATGTACAGAATACTTGTACGCATTGTTCAAACCTGAAGGA
AATTTCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAATTGAGAGAAGAAGAA
GGTGATAAGTGTGAAAATTAAATGTGATAACCTTTGAACCTTGAATTTTGGAGATGTATTCC
CAACAGCAGAATGCAACTGTGGGCATTTCTTGTCTTATTTCTTTCCAGAGAACGTGGTTTTCA
TTTATTTTTTCCCTCAAAAGAGAGTCAAATACTGACAGATTCGTTCTAAATATATTGTTTCTGT
CATAAAATTATTGTGATTTCTGATGAGTCATATTACTGTGATTTTCATAATAATGAAGACAC
CATGAATATACTTTTCTTCTATATAGTTTCAGCAATGGCCTGAATAGAAGCAACCAGGCACCAT
CTCAGCAATGTTTTCTTCTTGTGTTGTAATTATTTGCTCCTTTGAAAATTAAATCACTATTAATT
ACATTAAAAATCAAATTGGATAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 452

MTSKFILVSFILAALSSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVHVKQ
VTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEATPIWIT
NQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLYWED
PDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEERLIEL
DQYLDKDHYTLLDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYNSRIQP
IIA VADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTDLYPLLC
HLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPHYGVSLGS
IIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Important features:**Signal Peptide:**

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372,
382-385, 389-392**Somatomedin B Domain:**

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

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FIGURE 453

GGCCGCCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCGTGAC
TATGGCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTGCT
GATGGCCGCCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCCTGACCAA
CCCAGAGAAGAGCAGCACCAAAGAAACGGAGAGAAAAGAAACCAAAGCCGAGGAGGAGCTGGA
TGCCGAAGTCCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGGCAGGC
TGTCCCTGCAGGATCCCACGTACGGCTGAATCTTCAGACTGGGGAAAGAGAGGCCAAAACCTCCA
ATATGAGGACAAGTTCGAAATAATTTGAAAGGCCAAAAGGCTGGATATCAACACCAACACCTA
CACATCTCAGGATCTCAAGAGTGCCTGGCAAATTCAGGAGGGGGCAGAGATGGAGAGTTC
AAAGGAAGACAAGGCCAAGGCAGGCTGAGGTAAAGCGGCTCTTCCGCCCCATTGAGGAACTGAA
GAAAGACTTTGATGAGCTGAATGTTGTCATTGAGACTGACATGCAGATCATGGTACGGCTGAT
CAACAAGTTCAATAGTTCCAGCTCCAGTTTGAAGAGAAGATTGCTGCGCTCTTTGATCTTGA
ATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGGTCTTCAAGTGGT
GATCAATGGGCTGAACAGCACAGAGCCCCCTCGTGAAGGAGTATGCTGCGTTTGTGCTGGGCGC
TGCCTTTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGGAGCCCTGCAGAAGCT
GCTGGTCATCCTGGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGTCCTGTTTGCCTGTG
CTCCCTGCTGCGCCACTTCCCCTATGCCCAGCGGCAGTTCCTGAAGCTCGGGGGGCTGCAGGT
CCTGAGGACCCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTGCGCGTGGTCACACTGCT
CTACGACCTGGTCACGGAGAAGATGTTGCGCGAGGAGGAGGCTGAGCTGACCCAGGAGATGTC
CCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAGGCCTGTGGGAACAGGGCTG
GTGCGAGATCACGGCCCACCTCCTGGCGCTGCCCCGAGCATGATGCCCCGTGAGAAGGTGCTGCA
GACACTGGGCGTCCTCCTGACCACCTGCCGGGACCGCTACCGTCAGGACCCCCAGCTCGGCAG
GACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTEGCCAGCCTGGAGCTGCAGGATGGTGA
GGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAACAGCTTGCTGAAGGAGCTGAGAT**AG**
AGGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGAGGCTGAGGGGTGCCAGCGTGGGTG
GGCTTCTCAGGCAGGAGGACATCTTGGCAGTGCTGGCTTGGCCATTAAATGGAAACCTGAAGG
CCAA
AA

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FIGURE 454

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEELD
AEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTNTY
TSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMVRLI
NKFSSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAFVLGA
AFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKLGGLQV
LRTLQVEKGTAVLAVRVVTLTYDLVTEKMFEEEEAEELTQEMSPKLOQYRQVHLLPGLWEQGW
CEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLASLELQDGE
DEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

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FIGURE 455

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCCAGGAGGAGGCAGT
GGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCCTA
CCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGGTGT
CTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCCTCCTTGCCCTGTCTGGAGGCTGCTAGAC
TCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGCCCCGTCTTG
TGGTTCCTCTCTACCTGGGGAAATAAGGTGCAGCGGCCATGGCTACAGCAAGACCCCCCTGGA
TGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTTCTCGCCA
ACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCAGGACCTGG
GAGCTGGGGCCGGGGAAGACGCCCGGTGCGATGACAGCAGCAGCCGCATCATCAATGGATCCG
ACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAACCAGCTCTACT
GCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCCACTGCAGGAAGAAAGTTT
TCAGAGTCCGTCTCGGCCACTACTCCCTGTCACCAGTTTATGAATCTGGGCAGCAGATGTTCC
AGGGGGTCAAATCCATCCCCACCCTGGCTACTCCACCCCTGGCCACTCTAACGACCTCATGC
TCATCAAACCTGAACAGAAGAATTTCGTCCCCTAAAGATGTCAGACCCATCAACGTCTCCTCTC
ATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAACCAAGAGCCCCCAAG
TGCACTTCCCTAAGGTCCTCCAGTGCTTGAATATCAGCGTGCTAAGTCAGAAAAGGTGCGAGG
ATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGACAAAGCAGGTAGAGACT
CCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCCT
GGGGAGATTACCCTTGTGCCCCGCCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTCA
CCAAGTGATCCAGGAAACCATCCAGGCCAACTCCTGAGTCATCCCAGGACTCAGCACACCGG
CATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAGACCCTCATTCCTTCCCAGAGA
TGTTGAGAATGTTTCATCTCTCCAGCCCCTGACCCCATGTCTCCTGGACTCAGGGTCTGCTTCC
CCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCCCTGGGAACAATTTCCAAAACCTGTCCAG
GGCGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGCTCAGGGCCCATCCCTT
CTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAACTGAGAAGTGGAACCAAAAAA

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FIGURE 456

MATARPPWMWVLCALITALLGVTEHVLANNVSCDHPSNTVPSGSNQDLGAGAGEDARSDDS
SSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLSPV
YESGQQMFQGVKSIPHPGYSHPGHSNDLMLIKLNRIRPTKDVRPINVSSHCP SAGTKCLVSG
WGTTKSPQVHFPKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGRDSCQGD SGGPVVCN
GSLQGLVSWG DYPCARPNRPGVYTNLCKFTKWIQETIQANS

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FIGURE 457

GCAGTCAGAGACTTCCCCTGCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCTTGCTTCCTGAACT
AGCTCACAGTAGCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCTCACCGCTGTAGGAATCCAGATGCAGG
CCAAGTACAGCAGCAGGAGGACATGCTGGATGATGATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTG
CCACAACTCGGCATCCAGAGCCCCGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGA
CCCTGCTGACTTTGTGCTTGGTGTCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTCAGTACTACCAGC
TCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGTTGCAATCTC
TTCAAGTCCAGAATATAAAGCTTGAGGAAGTCTGCAGCATGTGGCTGAAAACTCTGTCTGAGCTGTATAACA
AAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATA
AAGACAGCAAAAGTTGGGAGGACTGTAAATATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAAAC
AAGAAGACCTGGAATTTGCCGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGCGCC
CTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTGTTCCATATTATAATAGATG
TCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGA
AGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCG
AAGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAG
ACATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTGTTCCTGTT
CAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGCCAC
CAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGCTCTCTTTCTCTCAA
TGTCTAATATCACCTCCCTGTTTTTCATGTCTTCCTTACACTTGGTGGAATAAGAACTTTTTGAAGTAGAGGAAA
TACATTGAGGTAAACATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTAC
CAGCAAATACACAAGGAATTCTTTTTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCC
CATCTGCCTTGTCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA
GCATTCCCTTCTGTGTCCATTAAGACTCTGATAATTGTCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATAT
ATCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAGT
GAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCAGGT
ACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

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FIGURE 458

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLLI
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY
SEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKDCKEL
KRCVCERRAGMVKPESLHVPPETLGED

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FIGURE 459

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCGAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCAC
TGGCGGCCCCGCAACACTCCGTCTCACCCTCTGGGCCCCACTGCATCTAGAGGAGGGCCGTCTGT
GAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGTGGT
CAGCTGGGTGAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAGGGAA
GTGGGAGCCTCGAGCCCTCGGGTGGAAGCTGACCCCAAGCCACCCTTCACCTGGACAGGATGA
GAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGATGTTTA
TTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCAGCCTCGC
CCACCAAGGAGATCCAGGTAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCAGCCAACT
ACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGTGCTTTGAAG
ACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATCGCCCTGGTGA
ATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGGAGATGTTATGC
ACCTAGTGAAATTCCTTAAAGAAATTCCGGGGGGTGCCTGGTGGTGGCTCCTACGACG
ATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTGGGGAGTTCCTACG
CAAAACAACCTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGACCTCAGGGGTAAAA
GCCCCTTTGAGCAGTTCTTAAAGAACAGCCCAGACACAAACAAATACGAGGGATGGCCAGAGC
TGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGTGGCTGTGGCTCTTCCTCAG
CCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCGGCAGGGGCTGAGGAGGA
GGAGCAGGGGGTGTGCTGCGTGGAAGGTGCTGCAGGTCTTGCACGCTGTGTGCGCCTCTCCTC
CTCGGAAACAGAACCTCCCACAGCACATCCTACCCGGAAGACCAGCCTCAGAGGGTCTTCT
GGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTGAGGGACTGCTGACGGCTGGTCCTG
AGGAAGGACAACTGCCAGACTTGAGCCCAATTAAATTTTATTTTGGCTGGTTTTGAAAAA
AAAAAAAAAAAAA

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FIGURE 460

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCPA
NYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSGDV
MHLVKFLKEIPGGALVLVASYDDPGTKMNDESRLFSDLGSSYAKQLGFRDSWVFIGAKDLRG
KSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop) .

amino acids 184-191

N-glycosylation site.

amino acids 107-110

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FIGURE 461

AAACTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGGA
AACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCCTC
TAGAACCCGACCCACCACCATGAGGTCCTGCCTGTGGAGATGCAGGCACCTGAGCCAAGGCGT
CCAGTGGTCCTTGCTTCTGGCTGTCCTGGTCTTCTTTCTCTTCGCCTTGCCCTCTTTTATTAA
GGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCTCTACA
GTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTATGCAGA
GCCAGCGCCAGAGAACAAATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCACCGGAGA
CAGAGGAAAGGAGGCCAACCAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCACACAGCACA
GAGGGCAGCATGGAAGAGCCCAGAAAAAGAGAAAACCATGGTGAACACACTGTCACCCAGAGG
GCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCCAGGACACAAA
GACGACCCAAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACGGTGTGAGAGAA
GCACCAGGGCAAAGCGGCAACCACAGCCAAGACGCTCATTCCCAAAGTCAGCACAGAATGCT
GGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCACAGCAGTCATCCC
ACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCTTTCCAGAGCCCCACGACGCA
GAGAAACCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTGGGATTTTGAGGAAAA
ATACAGCTTCGAAATAGGAGGCCTTCAGACGACTTGCCCTGACTCTGTGAAGATCAAAGCCTC
CAAGTCGCTGTGGCTCCAGAACTCTTTCTGCCCAACCTCACTCTCTTCCTGGACTCCAGACA
CTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTTGCACCACCCTTTGGCTTCATGGAGCT
CAACTACTCCTTGGTGCAGAAGGTCGTGACACGCTTCCCTCCAGTGCCCCAGCAGCAGCTGCT
CCTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGCATCACCTGTGCCGTGGTGGGCAACGGGGG
CATCCTGAACAACTCCACATGGGCCAGGAGATAGACAGTCACGACTACGTGTTCCGATTGAG
CGGAGCTCTCATTAAGGCTACGAACAGGATGTGGGGACTCGGACATCCTTCTACGGCTTTAC
CGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAATCGGGGTTTCAAGAACGTGCCTCT
TGGGAAGGACGTCCGCTACTTGCACTTCCTGGAAGGCACCCGGGACTATGAGTGGCTGGAAGC
ACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTTTCTGGTTCAGGCACAGACCCCAGGA
AGCTTTTTCGGGAAGCCCTGCACATGGACAGGTACCTGTTGCTGCACCCAGACTTTCTCCGATA
CATGAAGAACAGGTTTCTGAGGTCTAAGACCCTGGATGGTGCCCACTGGAGGATATAACGCCC
CACCATGGGGCCCTCCTGCTGCTCACTGCCCTTCAGCTCTGTGACCAGGTGAGTGCTTATGG
CTTCATCACTGAGGGCCATGAGCGCTTTTCTGATCACTACTATGATACATCATGGAAGCGGCT
GATCTTTTACATAAACCATGACTTCAAGCTGGAGAGAGAAGTCTGGAAGCGGCTACACGATGA
AGGGATAATCCGGCTGTACCAGCGTCCTGGTCCCGGAACTGCCAAAGCCAAGAACTTGACCGGG
GCCAGGGCTGCCATGGTCTCCTTGCTGCTCCAAGGCACAGGATACAGTGGGAATCTTGAGAC
TCTTTGGCCATTTCCCATGGCTCAGACTAAGCTCCAAGCCCTTCAGGAGTTCCAAGGGAACAC
TTGAACCATGGACAAGACTCTCTCAAGATGGCAAATGGCTAATTGAGGTTCTGAAGTTCTTCA
GTACATTGCTGTAGGTCTGAGGCCAGGGATTTTTAATTAAATGGGGTGATGGGTGGCCAATA
CCACAATTCTGCTGAAAAACACTCTTCCAGTCCAAAAGCTTCTTGATACAGAAAAAAGAGCC
TGGATTTACAGAAACATATAGATCTGGTTTGAATTCAGATCGAGTTTACAGTTGTGAAATCT
TGAAGGTATTACTTAACTTCACTACAGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTC
TAGAAGGGTCTATACTTGTCTTGTCTTAAAGCTATTTGACAACTCTACGTGTTGTAGAAAA
TGATAATAATACAAATGATTGTTGTCCATGGAAAGGCAAATAAATTTTCTACAGTGAAAAAAA
AAAAAAA

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FIGURE 462

MRSCWLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKPK
SQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAWKS
PEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNQGQTRKLTASRTVSEKHQGKAA
TTAKTLIPKSQHRMLAPTGA VSTRTRQKGVTTAVIPPEKKPQATPPPAPFQSPTTQRNQRLK
AANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHFNQSEW
DRLEHFAPPPFGFMELNYSLVQKVVTFRPPVPQQQLLASLPAGSLRCITCAVVGNGGILNNSH
MGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFTAFLSLTQSLILGNRGFKNVPLGKD VRY
LHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFREALHMDRYLLLHPDFLRYMKNRFL
RSKTL DGAHWRIYRPTTGALLLLLTALQLCDQVSAYGFITEGHERFSDHYDYTSWKRLIFYINH
DFKLEREVWKRLHDEGIIRLYQRP GPGTAKAKN

Important features:**Cytoplasmic Domain:**

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

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FIGURE 463

GGGGGAGCTAGGCCGCGGCAGTGGTGGTGGCGGCGGCGCAAGGGTGAGGGCGGGCCCCAGAAC
CCCAGGTAGGTAGAGCAAGAAGATGGTGTCTTCTGCCCCCTCAAATGGTCCCTTGCAACCATGTC
ATTTCTACTTTTCCTCACTGTTGGCTCTCTTAAGTGTGTCCACTCCTTCATGGTGTGACAGCAG
TGAAGCATCTCCAAAACGTAGTGTGGGACACCATTTCCTTGAATAAAAATACGACTTCCTGA
GTACGTCATCCCAGTTCATTATGATCTCTTGATCCATGCAAACCTTACCACGCTGACCTTCTG
GGGAACCACGAAAGTAGAAATCACAGCCAGTCAGCCCACCAGCACCATCATCCTGCATAGTCA
CCACCTGCAGATATCTAGGGCCACCCTCAGGAAGGGAGCTGGAGAGAGGCTATCGGAAGAACC
CCTGCAGGTCTTGGAAACACCCCCCTCAGGAGCAAAATTGCACTGCTGGCTCCCCGAGCCCCCTCT
TGTCGGGCTCCCGTACACAGTTGTCTTCACTATGCTGGCAATCTTTCGGAGACTTTCCACGG
ATTTTACAAAAGCACCTACAGAACCAAGGAAGGGGAAGTGGAGTACTAGCATCAACACAATT
TGAACCCACTGCAGCTAGAATGGCCTTTCCTGCTTTGATGAACCTGCCTTCAAAGCAAGTTT
CTCAATCAAAATTAGAAGAGAGCAAGGCACCTAGCCATCTCCAATATGCCATTGGTGAAATC
TGTGACTGTTGCTGAAGGACTCATAGAAGACCATTTTGATGTCACTGTGAAGATGACACACCTA
TCTGGTGGCCTTCATCATTTCAGATTTTGAGTCTGTGAGCAAGATAACCAAGAGTGGAGTCAA
GGTTTCTGTTTATGCTGTGCCAGACAAGATAAATCAAGCAGATTATGCACTGGATGCTGCGGT
GACTCTTCTAGAATTTTATGAGGATTATTTTCAGCATACCGTATCCCCCTACCCAAACAAGATCT
TGCTGCTATTCCCGACTTTCAGTCTGGTGTCTGTAAGAACTGGGGACTGACAACATATAGAGA
ATCTGCTCTGTTGTTTGTATGCAGAAAAGTCTTCTGCATCAAGTAAGCTTGGCATCACAGTGAC
TGTGGCCCATGAAGTGGCCACCAGTGGTTTGGGAACCTGGTCACTATGGAATGGTGGAAATGA
TCTTTGGCTAAATGAAGGATTTGCCAAATTTATGGAGTTTGTGTCTGTCACTGTGACCCATCC
TGAAGTGAAGTTGGAGATTATTTCTTGGCAAATGTTTGGACGCAATGGAGGTAGATGCTTT
AAATTCTCACACCCTGTGTCTACACCTGTGGAAATCTGCTCAGATCCGGGAGATGTTTGA
TGATGTTTCTTATGATAAGGGAGCTTGTATTCTGAATATGCTAAGGGAGTATCTTAGCGCTGA
CGCATTTAAAGTGGTATTGTACAGTATCTCCAGAAGCATAGCTATAAAAAATACAAAAAACGA
GGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAGATGGTGTAAAAGGGATGGATGGCTT
TTGCTCTAGAAGTCAACATTCATCTTCATCCTCACATTGGCATCAGGAAGGGGTGGATGTGAA
AACCATGATGAACACTTGGACACTGCAGAGGGGTTTTCCCTAATAACCATCACAGTGAGGGG
GAGGAATGTACACATGAAGCAAGAGCACTACATGAAGGGCTCTGACGGCGCCCCGACATGG
GTACCTGTGGCATGTTCCATTGACATTCATCACCAGCAAATCCAACATGGTCCATCGATTTTT
GCTAAAAACAAAACAGATGTGCTCATCTCCAGAAAGAGGTGGAATGGATCAAATTTAATGT
GGGCATGAATGGCTATTACATTGTGCATTACGAGGATGATGGATGGGACTCTTTGACTGGCCT
TTTAAAGGAACACACAGCAGTCAGCAGTAATGATCGGGCAAGTCTCATTAACAATGCATT
TCAGCTCGTCAGCATTGGGAAGCTGTCCATTGAAAAGGCTTGGATTATCCCTGTACTTGAA
ACATGAAACTGAAATTATGCCCGTGTTCAGGTTTGAATGAGCTGATTCCTATGTATAAGTT
AATGGAGAAAAGAGATATGAATGAAGTGGAACTCAATTCAAGGCCTTCCTCATCAGGCTGCT
AAGGGACCTCATTGATAAGCAGACATGGACAGACGAGGGCTCAGTCTCAGAGCAAATGCTGCG
GAGTGAACCTACTACTCCTCGCCTGTGTGCACAACATATCAGCCGTGCGTACAGAGGGCAGAAGG
CTATTTTCAGAAAGTGGAAAGGAATCCAATGGAACTTGAGCCTGCCTGTGACGTGACCTTGGC
AGTGTGTTGCTGTGGGGGCCCCAGAGCACAGAAGGCTGGGATTTTCTTTATAGTAAATATCAGTT
TTCTTTGTCCAGTACTGAGAAAAGCCAAATTGAATTTGCCCTCTGCAGAACCCAAAATAAGGA
AAAGCTTCAATGGCTACTAGATGAAAGCTTTAAGGGAGATAAAAATAAAACTCAGGAGTTTCC
ACAAATTTCTTACACTCATTGGCAGGAACCCAGTAGGATACCCACTGGCCTGGCAATTTCTGAG
GAAAAACTGGAACAACTTGTACAAAAGTTTGAAGTGGCTCATCTTCCATAGCCCCACATGGT
AATGGGTACAACAAATCAATTCTCCACAAGAACACGGCTTGAAGAGGTAAAAGGATTCTTCAG
CTCTTTGAAAGAAAATGGTTCTCAGCTCCGTTGTGTCCAACAGACAATTGAAACCATTTGAAGA
AAACATCGGTTGGATGGATAAGAATTTGATAAAATCAGAGTGTGGCTGCAAAGTGAAGAGCT
TGAACGTATGTAATAAATTCCTCCCTTGCCCGGTTCTGTTATCTCTAATCACCAACATTTTGT
TGAGTGTATTTTCAAAGTAGAGATGGCTGTTTTGGCTCCAACTGGAGATACTTTTTTCCCTTC
AACTCATTTTTTGGACTATCCCTGTGAAAAGAATAGCTGTAGTTTTTTCATGAATGGGCTTTTT
CATGAATGGGCTATCGCTACCATGTGTTTTGTTTCATCACAGGTGTTGCCCTGCAACGTAAACC
CAAGTGTGGGTTCCCTGCCACAGAAGAATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

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FIGURE 464

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVHY
DLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLOVLEHP
PQEQIALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTAARM
AFPCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVAFIIS
DFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAAIPDFQ
SGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWWNDLWLNNEG
AKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFDDVSYDKG
ACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMDFCSRSQHS
SSSSHHWQEGVDVKTMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPDTGYLWHVPL
TFITSKSNMVRFLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSLTLGLLKGTHTA
VSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIPMYKLMEKRDMN
EVETQFKAFLIRLLRDLIDKQTTWTDEGSVSEQMLRSELLLLACVHNYQPCVQRAEGYFRKWKE
SNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSTEKSQIEFALCRTQNKEKLQWLLD
ESFKGDKIKTQEFQILTLIGRNPVGYPLAWQFLRKNWNKLVQKFELGSSSIAHMVMGTTNQF
STRTRLEE VKGFFSSLKENGSQLRCVQQTITETIEENIGWMDKNFDKIRVWLQSEKLERM

Important features:**Signal peptide:**

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

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FIGURE 465

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCACT
GCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGA
CCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACAC
GTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGC
CAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTA
CACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGC
CCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGGAAGGCTG
TCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCT
CAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGG
TTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGAACTGCAATAG
GAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGA
ACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGAC
GCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGT
TGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTC
CTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAA
CTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCTACCTGTGTGCAGCC
CCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTA
TGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGT
GGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGA
GAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC
TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTC
CTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACCTCCCTC
TGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATCTGTCCATGAATCATCTT
CCCCACACACAATCATTATATCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGAGCATC
CGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTATCTGATAATACAGAC
CCTGTCCTTTCA

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FIGURE 466

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLMLIE
SGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQPPA
DPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCMPQPGCNLLN
GTQEIGPVGMTENCNRKDFTLCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETLLIID
VGLTSTLVGKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLNSLPPQ
AAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSS
FLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC

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FIGURE 467

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTTG
AGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTGCAGGATGATGGTGGCCCTTCG
AGGAGCTTCTGCATTGCTGGTTCTGTTCTTGCAGCTTTTCTGCCCCCGCCGAGTGTAACCA
GGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGAGCAAGGGCTGGAAAA
ATGTACCCAAGCAACGAGGGGCATACATTCAAGAATTCCAAGAGTTCTCAAAAAATATATCTGT
CATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACTTGGCACT
GAGAGTTGAACGTGCCCAACGGGAGATTGACTACATAACAATACCTTCGAGAGGCTGACGAGTG
CATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAAGAGAAAAA
GATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTCTTTGAAAAT
AGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATAACTCTCCAAA
GGTGTACTTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAACATACGGGCATT
CATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTCTTGGCAGGGGAAC
AGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTTCATAACCAAGCAACTTCTAATGAGATAAT
CAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCAGGAGGGGTAGGCCG
AGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGTGGATGAGCATGGGCT
CTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTTCTCACAAAGATTGAGCCGGG
CACACTGGGAGTGGAGCATTCATGGGATACCCCATGCAGAAGCCAGGATGCTGAAGCCTCATT
CCTCTTGTGTGGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCAGGGCCCTCATCGCATCAC
CTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGCCCAACTTGTTCCTCCCAA
GAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGATAAGCAGCTCTATGCTGCGAA
TGAAGGAAACCAGATCATTTACAAACTCCAGACAAAGAGAAAGCTGCCTCTGAAGTAATGCAAT
TACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTCTACAGGACAGTGAGGCTATAGC
CCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAGAGTGTGTAGAAGTGGAATAACGT
ATGCCTCCTTTCCCAAATGTCAGTGCCTTAGGTATCTTCCAAGAGCTTAGATGAGAGCATATC
ATCAGGAAAGTTTCAACAATGTCCATTACTCCCCCAAACCTCCTGGCTCTCAAGGATGACCAC
ATTCTGATACAGCCTACTTCAAGCCTTTTGTCTTACTGCTCCCCAGCATTTACTGTAACCTCTG
CCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGCCCCTAATATTCACCACTGGCTTTTCTC
TCCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTTTTCAAATGTCTATTGATATTCTCCCATTTT
CACTGCCCCAACTAAAATACTATTAATATTTCTTTCTTTTCTTTTCTTTTCTTTTGTAGACAAGGT
CTCACTATGTTGCCCAGGCTGGTCTCAAACCTCCAGAGCTCAAGAGATCCTCCTGCCTCAGCCT
CCTAAGTACCTGGGATTACAGGCATGTGCCACCACACCTGGCTTAAAATACTATTTCTTATTG
AGGTTTAACTCTATTTCCCTAGCCCTGTCTTCCACTAAGCTTGGTAGATGTAATAATAAAA
GTGAAAATATTAACATTTGAATATCGCTTTCAGGTGTGGAGTGTGTCACATCATTGAATTC
TCGTTTACCTTTGTGAAACATGCACAAGTCTTTACAGCTGTCAATTCTAGAGTTTAGGTGAGT
AACACAATTACAAAGTGAAAGATACAGCTAGAAAATACTACAAATCCCATAGTTTTTCCATTG
CCCAAGGAAGCATCAAATACGTATGTTTGTTCACCTACTCTTATAGTCAATGCGTTTCATCGTT
TCAGCCTAAAATAATAGTCTGTCCCTTTAGCCAGTTTTCATGTCTGCACAAGACCTTTCAAT
AGGCCTTTCAAATGATAATTCCTCCAGAAAACAGTCTAAGGGTGAGGACCCCAACTCTAGCC
TCCTCTTGTCTTGCTGTCCTCTGTTTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTG
AGCAAAAAAAAAAAAAA

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FIGURE 468

MMVALRGASALLVLFLAAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQEF
SKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLLQE
AEEKKIRTLLNASCDNMLMGIKSLKIVKKMMDTHGSWMKDAVYNPKVYLLIGSRNNTVWEF
ANIRAFMEDNTKPAPRKQILTLQGTGQVIYKGFLEFFHNQATSNEIIKYNLQKRTVEDRMLL
PGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGLGVEHSWDTPCRSQ
DAEASFLLCGVLYVVYSTGGQGPFRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIHYNPRDK
QLYAWNEGNQIIYKLQTKRKLPLK

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FIGURE 469

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGGC
AGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCCTC
CTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGGCCTGTGAGCGGGATGTCCAGTGTGGG
GCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCTGGGG
CGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCAAGCAC
CACACCTGTCCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTACCGCTGC
TCCATGGACTTGAAGAACATCAATTTTTTAGGCGCTTGCCTGGTCTCAGGATACCCACCATCCT
TTTCTGAGCACAGCCTGGATTTTTATTCTGCCATGAAACCCAGCTCCCATGACTCTCCCAG
TCCCTACACTGACTACCCTGATCTCTTGTCTAGTACGCACATATGCACACAGGCAGACATA
CCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGGCTGTGGTGTG
AAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTAAATGGCAGAAA
GGACATTCCCCCTCCCCTCCCAGGTGACCTGCTCTCTTCTGGGCCCTGCCCCCTCTCCCCA
CATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGTGCATTGCTCAGAG
TCCCAGGTCCTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGGACCAATTTGTGGGT
AGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGACTCAAGATTGGCTCTT
CCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCAGGGAGGCCAATCAGCC
CCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGACCTGTGACCTTCTGCCA
GAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGTTAACCCTGAAGCCCCCA
ATTCCCACAGCTTTTCCATTAAAATGCAAATGGTGGTGGTTCAATCTAATCTGATATTGACAT
ATTAGAAGGCAATTAGGGTGTTTCTTAAACAACCTCCTTTCCAAGGATCAGCCCTGAGAGCAG
GTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGGTGGGAGCAAGGGACAGGGAGC
AGGGCAGGGGCTGAAAGGGGCACTGATTCAGACCAGGGAGGCAACTACACACCAACATGCTGG
CTTTAGAATAAAAGCACCAACTGAAAAA

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FIGURE 470

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEETCHPG
SHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Important feratures:**Signal peptide:**

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

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FIGURE 471

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAAAATGTCTTTCC
TCCAGGACCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGCTG
CTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGGCCC
TGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAAGCAA
AGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTTCCTCT
GTCGAGAGGAAGCTGCGGATCTGTCCTCCCTGAAAAGCATGTTGGACCAGCTGGGCGTCCCCC
TCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTATTTCAAAG
GAGAAATCTTCCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGATGATGTTTA
TGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTTCCGAGCCTGGAACGGAGGCTTCTCTG
GAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTTCGTGGTGGGATCAGGAAAGCAGG
GCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACTTTCTGTTCTGG
AAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAAATGATTGTGTGAAACTG
CCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTCATGGGATGTATTGTTTCCACTCGTG
TCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTATTAATGTATTTTAA
TATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGACAAAAATCTGAAAAA
CTAATGAGGATTATTAAGCTAAACCTGGGAAATAGGAGGCTTAAAATTGACTGCCAGGCTGG
GTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGAGCAAGTCACTTGAG
GTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTCTCTACTAAAAATACAAAA
ATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCGGGAGGCTGAGGCAGGAGAA
TCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCACACCACTGTATTCCAGCCTG
GGTGACTGAGACTCTAACTAA

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FIGURE 472

MSFLQDPSFFTGMGWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLEKEPRT
FKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQP
YFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFGFILGGVFVVG
GKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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FIGURE 473

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTTT
TGGGATTTTAATTTTCAAACACAGCAGAAATGACATTTTTTCTGTCACTATTATTATTGTTGGT
ATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATC
AAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTCCTAC
CAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTT
AATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATGATTGTA
AATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATATATACAA
TAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACTTTATTAAT
TTTTAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGATCATATAAT
TTGATACAAATAAAAGAAAAGTGTTCTCTCCCCTTACAGAATTGACATTTTAAATGCGATACA
GTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAAAGAAGGGAAAA
TGTTGCCAAGGAAAAAAAAA

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FIGURE 474

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGKG
IVKGRNLDSRGLILGAEAWGRGVKKNT

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FIGURE 475

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTACCAAGAGCTGGAGACACCAT
CTCCACCGAGAGTCAATGGGCCCCATTGGCCCTGCACCTCCTCGTCCTCGTCCCCATCCTCCTC
AGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGCATG
CAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGGCTCAATCGGACCCTGAAG
CCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGCTCAGC
GATGCTGGACACAAGGTCACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATCTTCACC
TACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCCAGCTCTCAC
AGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTCACCCAGTACGAC
AAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAGAAGGTGCCC
GAGAAGCTGGGCTACGCCTTGCGTCCCCAGGAAAAGGGCCACTCGCCCGAAGACATCTACCAG
ATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGGCGATGAAGAAG
TTTGAAAGGCACACGCTCTTGGAATATCTTCTCGGGGAGGGGAACCTGAGCCGGCCGGCCGTG
CAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTTCGCCGAGGCCCTC
CGGGCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGGGTGGCTGGGACCTG
CTGCCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAACGCGCCCGTGGTGGCG
ATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCCCCGGCGCGGAATCTG
AAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGGCGGTGAAGCGCATCACC
TTCTCGCCGCCGCTGCCCCGCCACATGCAGGAGGCGCTGCGGAGGCTGCACTACGTGCCGGCC
ACCAAGGTGTTCTTAAGCTTCCGCAGGCCCTTCTGGCGCGAGGAGCACATTGAAGGCGGCCAC
TCAAACACCGATCGCCCGTCGCGCATGATTTTCTACCCGCCGCGCGAGGGCGCGCTGCTG
CTGGCCTCGTACACGTGGTCGGACGCGCGGCGGACGCTTCGCCGGCTTGAGCCGGGAAGAGGCG
TTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCCTGTCGTGCGCCAGCTCTGGGAC
GGCACCGGCGTCGTCAAGCGTTGGGCGGAGGACCAGCACAGCCAGGGTGGCTTTGTGGTACAG
CCGCCGGCGCTCTGGCAAACCGAAAAGGATGACTGGACGGTCCCTTATGGCCGCATCTACTTT
GCCGGCGAGCACACCGCCTACCCGCACGGCTGGGTGGAGACGGCGGTCAAGTCGGCGCTGCGC
GCCGCCATCAAGATCAACAGCCGGAAGGGGCTGCATCGGACACGGCCAGCCCCGAGGGGCAC
GCATCTGACATGGAGGGGCAGGGGCATGTGCATGGGGTGGCCAGCAGCCCCTCGCATGACCTG
GCAAAGGAAGAAGGCAGCCACCCTCCAGTCCAAGGCCAGTTATCTCTCCAAACACGACCCAC
ACGAGGACCTCGCATTAAAGTATTTTCGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 476

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRVI
VVGAGVAGLVAAKVLS DAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRILHK
LCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVP EKLGYALRPQEKGHSPEDIYQMALNQ
ALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMS EDGFFYLSFAEALRAHSC
LSDRLQYSRIVGGWDL LPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNLKVLKA
DVVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRPFWRREEHIEGGHSNTDR
PSRMIFYPPPREGALLASYTWS DAAAAFAGLSREEALRLALDDVAALHGPVVRQLWDGTGVV
KRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKSALRAAIKI
NSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQQLSLQNTTHTRTSH

Important features:

Signal peptide:

amino acids 1-21

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FIGURE 477

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAT
GGACGCTCTGAAGCCACCCTGTCTCTGGAGGAACACGAGCGAGGGAAGAAGGACAGGGACTCGTGTGGCAGGAA
GAACTCAGAGCCGGGAAGCCCCATTCACTAGAAAGCACTGAGAGATGCGGGCCCCCTCGCAGGGTCTGAATTTCCCT
GCTGCTGTTTCAAAAGATGCTTTTTATCTTTAACTTTTTGTTTTCCCCACTTCCGACCCCGGCGTTGATCTGCAT
CCTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACCAGACCTCAACCCGCTTACCTCTTCTTGACCTGAA
CAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGGTTTCCCAGAAGAACAATGACCTAACAAGTTGCTG
CTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTGCTTGGG
ATATAGAAAACCAACCAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTC
CTGTCTCTTGATATAAAGGTTATAAATCATCACCAGACCAGTTTGTGCGCATCTTTGCTCAGAAATAGGCCAGAGTG
GATCATCTCCGAATTGGCTTGTACACGTAATCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAAGC
CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAAGGCATTGGTGCTGAT
AGGGAATGTAGAGAAAGGCTTCACCCCGAGCCTGAAGGTGATCATCTTATGGACCCCTTTGATGATGACCTGAA
GCAAGAGGGGAGAGAGTGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAAGAGCACTTCAG
AAACCTGTGCCTCCTAGCCCAGAAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAGG
AGCCATGATAACCCATCAAAATATTGTTTTCAAATGCTGCTGCCTTTCTCAAATGTGTGGAGCATGCTTATGAGC
CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAGAGGATTGTACAGGCTGTTGTGTA
CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
CACATTGTTTTCCCGCGGTGCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCCTT
GAAGAAGTTCTTGTGAAGCTGGCTGTTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG
TTTTCTGGGACAAGCTCATCTTGTCAAAGATCCAGGACAGCCTGGGCGGAAGGGTTTCGTGAATTTGCTACTGGAGC
TGCCCCCATGTCCACTTCAGTCATGACATTCTTCCGGGCAGCAATGGGATGTGAGGTGTATGAAGCTTATGGTCA
AACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGACTGGACATCAGGTACGTTGGGGTGCCCCCTGGC
TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACACTTTACAGTGAATAATGAAGGAGAGGTCTGCAT
CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCTGAGAAGACACAGGAAGCCCTGGACAGTGATGGCTG
GCTTCACACAGGAGACATTGGTTCGCTGGCTCCCGAATGGAACCTGAAGATCATCGACCGTAAAAAGAACATTTT
CAAGCTGGCCCCAAGGAGAATACATTGCACCAGAGAAGATAGAAAATATCTACAACAGGAGTCAACCAAGTGTACA
AATTTTTGTATACCGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTCTTGACACAGATGTACTTCCCTC
ATTTGCAGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAACTGTGCCAAAACCAAGTTGTAAGGGGAAGCCATTTT
AGAAGACTTGCAGAAAATTGGGAAAGAAAGTGGCCTTAAAACCTTTTGAACAGGTCAAAGCCATTTTTCTTCATCC
AGAGCCATTTTTCCATTGAAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTTCCAAATACTT
TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGGCCCCACTG
TGCATGCTTGTGAGAAAATGGATTAAAAACTATTCTTACATTTGTTTTGCCTTTCCCTCCTATTTTTTTTTTAACC
TGTTAAACTCTAAAGCCATAGCTTTTGTTTTATATTGAGACATATAATGTGTAAACTTAGTTCCCAATAAATCA
ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTTCAA
GATCCAGTTTTATGTTCTGTGTCCTTCCTCATGATTTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT
CAAAGGGACCCTCTGTGCCTTCTTCTTTGTTTTGTGATAAACATAACTTGCCAACAGTCTCTATGCTTATTTACA
TCTTCTACTGTTCAAACCTAAGAGATTTTTAAATTCTGAAAACTGCTTACAATTATGTTTTCTAGCCACTCCAC
AAACCACTAAAATTTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT
CTGCGTAAATTAAATTGTGTACTGAAGGGAAAAGTTTGATCATACCAAACATTTTCTAAACTCTCTAGTTAGATA
TCTGACTTGGGAGTATTAATAAATGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTTAAAGCATTATTTA
CAGTAGGAACCTGGGGAGTAAATCTGTTCCCTACAGTTTGCTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA
GGTGGGCCCAGTGAACCTTTCCAGTAAATGAAGCAAGCACTGAATAAAAACCTCCTGAACTGGGAACAAAGATCT
ACAGGCAAGCAAGATGCCACACAACAGGCTTATTTTCTGTGAAGGAACCAACTGATCTCCCCACCCTTGGATT
AGATTCTGCTCTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAATGTAAAGTCTTTAAAATAAAC
TATTACAGATAAAAAA

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FIGURE 478

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFNF
LFSPLPTPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARKGVSQKNNDLTSCC
FSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYSKSSPDQ
FVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKALVLIG
NVEKGFTPSLKVIIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPEDLSVIC
FTSGTTGDPKGAMITHQNIVSNAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQAVVYSC
GARVGFFQGDIRLLADDMKTLKPTLFPAPVPRLLNRIYDKVQNEAKTPLKKFLLKLAVSSKFKE
LQKGIIRHDSFWDKLIFAKIQDSLGRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGQTEC
TGGCTFTLPGDWTS GHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFKGYLKDPEKT
QEALDSGDWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNRSQPVLOIFVH
GESLRSSLVGVVVPD TDVLP SFAAKLG VKGSFEELCQNQVVREAILEDLQKIGKESGLKTFEQ
VKAIFLHPEPFSIENGLLTPTLKAARGELSKYFRTQIDSLYEHIQD

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

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FIGURE 479

GGAGGCGGAGGCCGCGGCGAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGCCCCGAGCGGGGC
CCGGGGCCCCCTAAGCCATTTCCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAATCC
GGTATGGACGACTGGAAGCCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGGAGC
TGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTGACACA
GGGGCCGTGCTTTTCCTGCTGGTGACTGTCATTGTCAATATCAAGTTGATCCTGGACACTCGG
CGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCCCTAGGC
CGCCTGGAGCCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTGGACGTAGAGGTGTAT
TCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATGAGGCCCGG
GAGCAGGGCCCGGGGCATCCATGTCATTGTCTCAACCAGGCCACGGGCCACGTGATGGCAAAA
CGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTCAACATGGTA
GCGCCCCGGCCGAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACCTCAAGGACACA
GCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGCTGGAGGGACACA
TGGGCCTTCGTGGGACGAAAAGGAGGTCCTGTCTTCGGGGAGAAACATTCTAAGTCACCTGCC
CTCTCTTCCTGGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGAGCTCAGCAGAAGAG
GCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGCTTCTGCAGCAAAGTT
GAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGAGTTCAGCCCTGACCCA
CTCCCAGACAACAAGGTCCTCAATGTGCCTGTGGCTGTCATTGCAGGGAACCGACCCAATTAC
CTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCCAGGGGGTGTCTCCTCAGATGATAACAGTT
TTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACTGTTTGGTCTGAGGGGCATC
CAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGCACTACAAGGCCAGCCTCACT
GCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGCTGTGGTTCTGGAAGAGGACCTGGACATT
GCTGTGGATTTTTTTCAGTTTTCCTGAGCCAATCCATCCACCTACTGGAGGAGGATGACAGCCTG
TACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACACGGCTGAGGACCCAGCACTACTG
TACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTCAGGAGGTCCTTGTAACAAGGAGGAG
CTTGAGCCCCAAGTGGCCTACACCGGAAAAGCTCTGGGATTGGGACATGTGGATGCGGATGCCT
GAACAACGCCGGGGGCCGAGAGTGCATCATCCCTGACGTTTCCCGATCCTACCACTTTGGCATC
GTCGGCCTCAACATGAATGGCTACTTTCACGAGGCCTACTTCAAGAAGCACAAAGTTCAACACG
GTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCTGAAGAAAGAAGCTTATGAAGTGGAAAGTT
CACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACCACAGCAAGAACCCTTGTGAAGACTCTTTC
CTGCCAGACACAGAGGGCCACACCTACGTGGCCTTTATTTCGAATGGAGAAAGATGATGACTTC
ACCACCTGGACCCAGCTTGCCAAGTGCCTCCATATCTGGGACCTGGATGTGCGTGGCAACCAT
CGGGGCCTGTGGAGATTGTTTTCGGAAGAAGAACCCTTCCTGGTGGTGGGGGTCCCGGCTTCC
CCCTACTCAGTGAAGAAGCCACCCTCAGTCACCCCAATTTTCTGGAGCCACCCCCAAAGGAG
GAGGGAGCCCCAGGAGCCCCAGAACAGACATTGAGACCTCCTCCAGGACCTGCGGGGCTGGGT
ACTGTGTACCCCCAGGCTGGCTAGCCCTTCCCTCCATCCTGTAGGATTTTGTAAGATGCTGGTA
GGGGCTGGGGCTACCTTGTTTTTAACATGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCC
CTGCTCCAACACCCCGTTCTGAGTTAAAAGTCTATTTATTTACTTCCTTGTTGGAGAAGGGC
AGGAGAGTACCTGGGAATCATTACGATCCCTAGCAGCTCATCCTGCCCTTTGAATACCCTCAC
TTTCCAGGCCTGGCTCAGAATCTAACCTATTTATTGACTGTCTGAGGGCCCTTGAAAACAGGC
CGAACCTGGAGGGCCTGGATTTCTTTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTC
TTACTCAGGAACTGCTGTGCCCAACCCATGGACAGGCCCAGCTGGGGCCCACATGCTGACAC
AGACTCACTCAGAGACCCTTAGACACTGGACCAGGCCTCCTCTCAGCCTTCTCTTTGTCCAGA
TTTCCAAAGCTGGATAAGTTGGTCATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAA
AAAAAAAAAAAAAAAA

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FIGURE 480

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTVIVNIKLILDTRR
AISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEARE
QGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLFLNMVAPGRVLICTVKDEGSFHLKDTA
KALLRSLGSQAGPALGWRDWTAFVGRKGGPVFGEKHSKSPALSSWGDVPVLLKTDVPLSSAEEA
ECHWADTELNRRRRRRFC SKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPAVIAGNRPNYL
YRMLRSLLSAQGVSPQMITVFIDGYEEMPMDVVALFGLRGIQHTPISIKNARVSQHYKASLTA
TFNLFPEAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLY
RVETMPGLGWVLRSLYKEELEPKWPTPEKLWDWDMWMMRMPEQRRGRECIIPDVSRSYHFGIV
GLNMNGYFHEAYFKKHKFNTVPGVQLRNVDSLKKEAYEVEVHRLLEAEVLDHHSKNPCEDSFL
PDTEGHTYVAFIRMEKDDDDFTTWTQLAKCLHIWDLVDRGNHRGLWRLFRKKNHFLVVGVPASP
YSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

Important features:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

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FIGURE 481

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCA
GGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT
GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTT
CCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCA
TTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCA
GCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACCTCTGGAA
TTTTTAAAAATCCCTTCCACACTTGACACCACCCATGGACCCATCTGTGCCCATCTGGATTATT
ATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATC
TGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAA
AACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGGGGCATATTA
ATGATGCCTTCATTGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTC
CTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGAT
CATATATTTTGTTTCACCATTCCTTCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAG
CAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAA
AATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAA
GCATTTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAA
ATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTT
TGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTA
AATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGGAAATTTTATCCTGTTATCACACCA
ACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT
TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTTTAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 482

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVPN
REATEISHVLLCNVTQRVSFVFWVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTFLEFL
KIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKCENM
ITIENGIPSDPLDMKGGILMMPS

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FIGURE 483

CGTCTCTGCGTTTCGCC**ATG**CGTCCCGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGGGC
CCTGGCTTGGGGCCGTGGGCTTTCGTGAGCTCCATGGGCTCGGGGAACCCCGCGCCCGGTGGTGT
TTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTGTCTCCAGACTGATGTCACCCG
GGCCGAGTGCTGTGCCTCCGGCAACATTGACACCGCCTGGTCCAACCTCACCCACCCGGGGAA
CAAGATCAACCTCCTCGGCTTCTTGGGCCTTGTCCACTGCCTTCCCTGCAAAGATTTCGTGCGA
CGGCGTGGAGTGCGGCCCCGGGCAAGGCGTGCCGCATGCTGGGGGGCGCCCGCGCTGCGAGTG
CGCGCCCGACTGCTCGGGGCTCCCGGCGCGGCTGCAGGTCTGCGGCTCAGACGGCGCCACCTA
CCGCGACGAGTGCGAGCTGCGCGCCGCGCGCTGCCGCGGCCACCCGGACCTGAGCGTCATGTA
CCGGGGCCGCTGCCGCAAGTCTGTGAGCACGTGGTGTGCCCCGCGGCCACAGTCGTGCGTTCGT
GGACCAGACGGGCAGCGCCCACTGCGTGGTGTGTGAGCGGCGCCCTGCCCTGTGCCCTCCAG
CCCCGGCCAGGAGCTTTGCGGCAACAACAACGTACCTACATCTCCTCGTGCCACATGCGCCA
GGCCACCTGCTTCTGGGCCGCTCCATCGGCGTGCGCCACGCGGGCAGCTGCGCAGGCACCCC
TGAGGAGCCGCCAGGTGGTGAAGTCTGCAGAAGAGGAAGAGAAGTTCGT**GTGA**GCCTGCAGGAC
AGGCCTGGGCCTGGTGCCCCGAGGCCCCCCATCATCCCCTGTTATTTATTGCCACAGCAGAGTC
TAATTTATATGCCACGGACACTCCTTAGAGCCCGGATTCGGACCACTTGGGGATCCCAAGACC
TCCCTGACGATATCCTGGAAGGACTGAGGAAGGGAGGCCTGGGGGGCCGGCTGGTGGGTGGGAT
AGACCTGCGTTCCGGACACTGAGCGCCTGATTTAGGGCCCTTCTCTAGGATGCCCCAGCCCT
ACCCTAAGACCTATTGCCGGGGAGGATTCCACACTTCCGCTCCTTTGGGGATAAACCTATTAA
TTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGGTAATTCCTGAAGAGGCATGACTGC
TTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGTGTACGGA
GGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGT
GAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAGCCTGGGTGAGTATGGAGGGTCT
AGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGAGTAT
GGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTG
GGTGTGTACGGAGGGTCTAGTCTGAGTGCGTGTGGGGACCTCAGAACACTGTGACCTTAGCCC
AGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGCTGCCACCATTCCCTGCCAGCCCAAGAACT
CCAGCTTCCCCACTGCCTCTGTGTGCCCCCTTTCGCTCCTGTGAAGGCCATTGAGAAATGCCCA
GTGTGCCCCCTGGGAAAGGGCACGGCCTGTGCTCCTGACACGGGCTGTGCTTGGCCACAGAAC
CACCCAGCGTCTCCCCTGCTGCTGTCCACGTCAGTTCATGAGGCAACGTCGCGTGGTCTCAGA
CGTGGAGCAGCCAGCGGCAGCTCAGAGCAGGGCACTGTGTCCGGCGGAGCCAAGTCCACTCTG
GGGAGCTCTGGCGGGGACCACGGGCCACTGCTCACCCACTGGCCCCGAGGGGGGTGTAGACG
CCAAGACTCACGCATGTGTGACATCCGGAGTCCTGGAGCCGGGTGTCCAGTGGCACCACTAG
GTGCCTGCTGCCTCCACAGTGGGGTTACACCCAGGGCTCCTTGGTCCCCCACAACCTGCCCC
GGCCAGGCCTGCAGACCCAGACTCCAGCCAGACCTGCCTCACCCACCAATGCAGCCGGGGCTG
GCGACACCAGCCAGGTGCTGGTCTTGGGCCAGTTCTCCACGACGGCTCACCCCTCCCTCCAT
CTGCGTTGATGCTCAGAATCGCCTACCTGTGCCTGCGTGTAAACCACAGCCTCAGACCAGCTA
TGGGGAGAGGACAACACGGAGGATATCCAGCTTCCCCGGTCTGGGGTGAGGAATGTGGGGAGC
TTGGGCATCCTCCTCCAGCCTCCTCCAGCCCCAGGCAGTGCCTTACCTGTGGTGCCCCAGAAA
AGTGCCCTAGGTTGGTGGGTCTACAGGAGCCTCAGCCAGGCAGCCACCCACCCCTGGGGCC
CTGCCTCACCAAGGAAATAAAGACTCAAGCCATAAAAAAA

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FIGURE 484

MRPGAPGPLWPLPWGALAWAVGFVSSMSGSGNPAPGGVCWLQQGQEATCSLVLQTDVTRAECCA
SGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVCEGPGKACRMLGGRPRCECAPDCS
GLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSCEHVVCPRPQSCVVDQTGS
AHCVVCRAAPCPVPSSPGQELCGNNNVITYISSCHMRQATCFLGRSIGVRHAGSCAGTPEEPPG
GESAEEEENFV.

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation sites.

amino acids 73-77, 215-219

Osteonectin domain proteins.

amino acids 97-130, 169-202

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FIGURE 485

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCCC
GAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGGA
AACGGGCGTTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATCATC
GTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGATCATG
GAGCTGGAAGGCAGGGTCCGCAGGGCGGGCTGCAGAGAGAGGGCGCCGTGGAGCTGAAGAAGAAC
GAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGCCACAAC
TTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTTGGTGAATAACATC
ACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGAGGAATTAC
GGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAGAGGAAGTTC
TCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTGTGAGGAGCGA
ATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGAGTGAAAACAAC
GACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAGGCAGCAGGCCTG
CCACACACAGAGGTGCCACAAGGGAAGGGAAACGTGCTTGGTAACAGCAAGTCCCAGACACCA
GCCCCCAGTTCCGAAGTGGTTTTTGGATTCAAAGAGACAAGTTGAGAAAGAGGAAACCAATGAG
ATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAGCCAGGCCGGGAGCAG
GTGGTGGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGGAGAACTGGGCCAGACC
CCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGATGGAGGGCCCTGAGCGA
GACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCTGCCGGGGAAGGGAGAAAC
CAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAATGAAGCAGAATCTGAGACA
GACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATGTTTTTAATGTTGAAGATCAG
AAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGGAATCATACACTCTTGAATTGAA
CTGGAATCACATATTTTCAACAGGGCCGAAGAGATGACTATAAAATGTTTCATGAGGGACTGA
ATACTGAAAACGTGTGAAATGTACTAAATAAAATGTACATCTGA

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FIGURE 486

MMGLGNGRRSMKSPPLVLAALVACIIVLGFNWYIASSRSVDLQTRIMELEGRVRRAAAERGAV
ELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQLKT
LQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVASRD
LSENNDQRQQLQALSEPQPRQLQAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLDSCRQVEK
EETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQENPEM
EGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGNDRNIDVF
NVEDQKRDTINLLDQREKRNHTL

Important features:**Signal peptide:**

amino acids 1-29

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FIGURE 487

AACTCAAACCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGGG
TGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTCATGTAT
GGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGGCCT
ATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGCTCGG
TTAAAATGCACTTTCTCCAGCTTTGCCCCCTGTGGGTGATGCTCTAACAGTGACCTGGAATTTT
CGTCCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTCCAACCC
ATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGATGCCTCC
ATCCTTCTCTGGAAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGAAGAACCCA
CCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTACGCTTCTCT
GAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCATAATAGTAATT
GTAGTGGTCCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTCATAAAGTGGTG
GAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCTGTTTATTTAGAA
GACACAGACTAAACAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAAGAACCCTAGTATT
TCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGTTTCCAACCAGTTC
TGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCACAGTGCTCCTCCATAT
CACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCAGAGTGTAATTTTTTCAA
GTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTTTGCCCTTAAGACACTACTTACAGTGT
TATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCCAATTTGTCTGTACATTT
CCTTTCACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTAATGTGTTTACTCTCTTTCC
TTCCCACATTCTCAATTAAAGGTGAGCTAAGCCTCCTCGGTGTTTCTGATTAACAGTAAATC
CTAAATTCAAACGTGTTAAATGACATTTTTATTTTTATGTCTCTCCTTAACATATGAGACACATC
TTGTTTTACTGAATTTCTTTCAATATTCAGGTGATAGATTTTTTGTCG

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FIGURE 488

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVTW
NFRPLDGGPEQFVFYYHIDPFQPMSEGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQVK
NPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLQHYRKKRWAERAHK
VVEIKSKEEERLNQEKKVSVYLETD

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FIGURE 489

AAGCAACCAAAGCTGCAAGCTTTGGGAGTTGTTGCTGTCCCTGCCCTGCTCTGCTAGGGAGAG
AACGCCAGAGGGGAGGCGGCTGGCCCCGGCGGCAGGCTCTCAGAACCCTACCGGCGGATGCTACT
GCTGTGGGTGTGCGGTGGTCGCAGCCTTGGCGCTGGCGGTACTGGCCCCGGAGCAGGGGAGCA
GAGGCGGAGAGCAGCCAAAGCGCCCAATGTGGTGTGCTGGTCTGTGAGCGACTCCTTCGATGGAAG
GTTAACATTTTCATCCAGGAAGTCAGGTAGTGAACTTCCTTTTATCAACTTTATGAAGACACG
TGGGACTTCCTTTCTGAATGCCTACACAACTCTCCAATTTGTTGCCCATCACGCGCAGCAAT
GTGGAGTGGCCTCTTCACTCACTTAACAGAATCTTGAATAATTTTAAGGGTCTAGATCCAAA
TTATACAACATGGATGGATGTCATGGAGAGGCATGGCTACCGAACACAGAAATTTGGGAACT
GGACTATACTTCAGGACATCACTCCATTAGTAATCGTGTGGAAGCGTGGACAAGAGATGTTGC
TTTCTTACTCAGACAAGAAGGCAGGCCCATGGTTAATCTTATCCGTAACAGGACTAAAGTCAG
AGTGATGGAAAGGATTGGCAGAATACAGACAAAGCAGTAACTGGTTAAGAAAGGAAGCAAT
TAATTACACTGAACCATTTGTTATTTACTTGGGATTAAATTTACCACACCCTTACCCTTCACC
ATCTTCTGGAGAAAATTTTGGATCTTCAACATTTACACATCTCTTTATTGGCTTGAAAAAGT
GTCTCATGATGCCATCAAAATCCCAAAGTGGTCACCTTTGTGAGAAATGCACCCTGTAGATTA
TTACTCTTCTTATACAAAAAAGTGCCTGGAAGATTTACAAAAAAGAAATTAAGAATATTAG
AGCATTTTATTATGCTATGTGTGCTGAGACAGATGCCATGCTTGGTGAAATTTTGGCCCT
TCATCAATTAGATCTTCTTCAAGAACTATTGTATATACTCCTCAGACCATGGAGAGCTGGC
CATGGAACATCGACAGTTTTATAAATGAGCATGTACGAGGCTAGTGCACATGTTCCGCTTTT
GATGATGGGACCAGGAATTAAGCCGGCCTACAAGTATCAAATGTGGTTTCTCTTGTGGATAT
TTACCCTACCATGCTTGATATTGCTGGAATTCCTCTGCCTCAGAACCTGAGTGGATACTCTTT
GTTGCCGTTATCATCAGAAACATTTAAGAATGAACATAAAGTCAAAAACCTGCATCCACCCTG
GATTCTGAGTGAATTCATGGATGTAATGTGAATGCCTCCACCTACATGCTTCGAACTAACCA
CTGGAATATATAGCCTATTCGGATGGTGCATCAATATTGCCTCAACTCTTTGATCTTTCCTC
GGATCCAGATGAATTAACAAATGTTGCTGTAAAATTTCCAGAAATTACTTATTCTTTGGATCA
GAAGCTTCATTCCATTATAAAGTACCCTAAAGTTTCTGCTTCTGTCCACCAGTATAATAAAGA
GCAGTTTATCAAGTGGAAACAAAGTATAGGACAGAATTATTCAAACGTTATAGCAAATCTTAG
GTGGCACCAAGACTGGCAGAAGGAACCAAGGAAGTATGAAAATGCAATTGATCAGTGGCTTAA
AACCCATATGAATCCAAGAGCAGTTTGAACAAAAAGTTTAAAAAATAGTGTCTAGAGATACAT
ATAAATATATTACAAGATCATAATTATGTATTTTAAATGAAACAGTTTAAATAATTACCAAGT
TTTGGCCGGGCACAGTGGCTCACACCTGTAATCCCAGGACTTTGGGAGGCTGAGGAAAGCAGA
TCACAAGGTCAAGAGATTGAGACCATCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAA
TACAAAAATTAGCTGGGCGCGGTGGTGCACACCTATAGTCTCAGCTACTCAGAGGCTGAGGCA
GGAGGATCGCTTGAACCCGGGAGGCAGCAGTTGCAGTGAGCTGAGATTGCGCCACTGTACTCC
AGCCTGGCAACAGAGTGAGACTGTGTGCAAAAAAATAAAAAATAAATAAATAAATTACCAA
TTTTTTCATTATTTTGTGAAGAATGTAGTGTATTTTAAAGATAAAATGCCAATGATTATAAAATCA
CATATTTTCAAAAATGGTTATTATTTAGGCCTTTGTACAATTTCTAACAATTTAGTGGAAGTA
TCAAAAGGATTGAAGCAAATACTGTAACAGTTATGTTCTTTAAATAAATAGAGAATATAAAAT
ATTGTAATAATATGTATCATAAAATAGTTGTATGTGAGCATTTGATGGTGAAAAA
AA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 490

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSDFGRSLTFHGPSQVVKLPFINFM
KTRGTSFLNAYTNSPICCPSSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQKF
GKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNWLRK
EAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLSEMHP
VDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIYSSDHG
ELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPLPQNLSG
YSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGASILPQLFD
LSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIGQNYSNVIA
NLRWHQDQWQKEPRKYENAIQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

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FIGURE 491

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGA
GCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGC
CTCTCTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGT
TGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGT
TGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGA
CATCTATAGCACCCCTTCTGGGCCTGCCCCGCTGACATCCAGGCTGCCCAGGCCATGATGGTGAC
ATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTT
CTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTCATCCTTGG
AGGCCTCCTGGGATTCTTCTGTTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTC
ACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTT
TTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCCCAGAGAAATCG
CTCCAATACTACGATGCCTACCAAGCCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGG
TCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGTATGTGTGAAAGAAC
CAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCA
CAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGGATAGACTGACTTTGG
CCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATGCAGGTTGAATTGCCAA
GGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTCCCCTGCCCTAAGTCCCC
AACCCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTTGCCCTCTGGT
TTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTGACTGACCCCTCTGTGATCAA
AGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGT
GGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC
TGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCCAGACTAATTTGTGCATGAACTG
AAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGACAGGAA
GGCAGCCTGGGACATTTAAAAAATA

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FIGURE 492

MASLGLQLVGYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQ
CDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIIISVVGMRCTVFCQESRAKDRVAVAGGVFFI
LGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQR
NRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSSYSLTGYV

Important features:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

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FIGURE 493

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGCT
TATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAGAA
CCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAGTGC
TGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCACCTTC
TGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTGTGAAG
CTGAAGGTTCAAGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGTGAAAGC
AGAAGACGTTTTCCCTTGAGAAAGACATAGAAAGAAAATCAACTTTCACTAAGGCATCTCAGAAA
CATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATGATGCAGCT
CCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGTAGATTATCA
GGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

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FIGURE 494

MVPRI FAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSET
RQCGPPCTFWPCFELCCLDSFGLTNDFVVKLVQGVNSQCHSSPISSKCESRRRFP

Important features:

Signal peptide:

amino acids 1-25

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FIGURE 495

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATTT
TCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCTGA
TGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCTGCAGCACTGTTGCT
ATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGAGTCT
GCTTTGAGCAGTGCTGCCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGACTCAG
CCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTCAGCTAATGGAACATCAGGGGAACGATGA
CTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTTACCTGAGATCTGGGA
TGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCCACTTCATTCTGTGACC
TGTCTGAGGCCCACCCTGCAGCTGCCCTGAGGAGGCCCACAGGTCCCCTTCTAGAATTCTGGA
CAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGATGACCCCTATG
GCCAACATCAACCCGGCACCAACCCCAAGGCTGGCTGGGGGAACCCTTCACCCTTCTGTGAGATT
TTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAATAAATTTATGTA
CTTTATAAATGAAAA

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FIGURE 496

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVPL
ARTQTCGNCTFRVC FEQCCPWTFMVKLINQNCDSARTSDDR LCRSVS

Important features:

Signal peptide:

amino acids 1-24

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FIGURE 497

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACTC
CTTGGCCTCCGCAGCCGATCACATGAAGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCCTGGC
ACAGGTGTGGCTGGTACCCGGCTTGGCCCCCAGTCCTCAGTCGCCAGAGACCCAGCCCCCTCA
GAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGGAGGAAGAGGAAGATGAGCAGGAGGCCAG
CGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTTGCCAA
GGAGACTTCAAACCTTCGGATTTCAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGGCAACAT
GGTCTTCTCTCCATTTGGCATGTCCTTGGCCATGACAGGCTTGATGCTGGGGGCCACAGGGCC
GACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAGCCCGGGCT
CCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCTCCCGCAACCTGGAAGTGGGCCTCTC
ACAGGGGAGTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCTTCAATTTATC
CAAGAGGTATTTTGATACAGAGTGCGTGCCTATGAATTTTCGCAATGCCTCACAGGCCAAAAG
GCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAATTCCCAAACCTGTTTGATGAGAT
TAATCCTGAAACCAAATTAATTCTTGTGGATTACATCTTGTTCAAAGGGGAAATGGTTGACCCC
ATTTGACCCTGTCTTCACCGAAGTCGACACTTTCACCTGGACAAGTACAAGACCATTAAGGT
GCCCATGATGTACGGTGCAGGCAAGTTTGCTCCACCTTTGACAAGAATTTTCGTTGTCATGT
CCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCATGGAGAAAATGGGTGA
CCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACATGGCTCAGAAACATGAA
AACCAGAAACATGGAAGTTTTCTTTCCGAAGTTCAAGCTAGATCAGAAGTATGAGATGCATGA
GCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCCTTTGCTGACCTTAGTGAACCTCTC
AGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGAACAGTGATTGAAGTTGATGA
AAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATTACTGCTTATTCCATGCCTCCTGT
CATCAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAGAAACCTCTGGAATGCTTCTGTT
TCTGGGCAGGGTGGTGAATCCGACTCTCCTATAATTCAGGACATGCATAAGCACTTCGTGCTG
TAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGATACCAGCAATGGATGGCAGGGGAG
AGTGTTCTTTTTGTTCTTAAGTAGTTTAGGGTGTCTCAAATAAATAACAGTAGTCCCCACTTA
TCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGCCTGAAACGGTGGACAGTGCTGAACCT
TATATATATTTTTTCTTACACATACATACCTATGATAAAGTTTAATTTATAAATTAGGCACAG
TAAGAGATTAAACAATAATAACAACATTAAGTAAAATGAGTACTTGAACGCAAGCACTGCAAT
ACCATAACAGTCAAACCTGATTATAGAGAAGGCTACTAAGTGACTCATGGGCGAGGAGCATAGA
CAGTGTGGAGACATTGGGCAAGGGGAGAATTACATCCTGGGTGGGACAGAGCAGGACGATGC
AAGATTCCATCCCCTACTCAGAATGGCATGCTGCTTAAGACTTTTAGATTGTTTATTTCTGG
AATTTTTTCATTTAATGTTTTTGGACCATGGTTGACCATGGTTAACTGAGACTGCAGAAAGCAA
AACCATGGATAAGGGAGGACTACTACAAAAGCATTAAATTGATACATATTTTTTAAAAAAA
AAAAAAA

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FIGURE 498

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E E
E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I K R
G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F D T E
C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P V F T E
V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L A L E D Y
L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A T G R N L Q
V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F L G R V V N P
T L L

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FIGURE 499

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGGCAACAGCTTGCGGCTGCGGGGAGCTCCCC
TGGGCGCTCCGCTGGCTGTGCAGGCGGCCATGGATTTCCTTGCGGAAAATGCTGATCTCAGTCG
CAATGCTGGGCGCAGGGGCTGGCGTGGGCTACGCGCTCCTCGTTATCGTGACCCCGGGAGAGC
GGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAGGAGCAGGGAGGAGGCGG
CCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAACGTGG
CCTGGAGGAAGAACTGGATGGTTGGCGGCGAAGGCGGCGCCAGCGGGAGGTCACCGTTGAGACC
GGACTTGCCTCCGTGGGCGCCGGACCTTGGCTTGGGCGCAGGAATCCGAGGCAGCCTTTCTCC
TTCGTGGGCCCAGCGGAGAGTCCGGACCGAGATACCATGCCAGGACTCTCCGGGGTCCTGTGA
GCTGCCGTCGGGTGAGCACGTTTCCCCCAAACCCTGGACTGACTGCTTTAAGGTCCGCAAGGC
GGGCCAGGGCCGAGACGCGAGTCGGATGTGGTGAAGTGAAGAACCAATAAAATCATGTTTCCT
CCAAA

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FIGURE 500

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLAT
LQEAATTQENVAWRKNWMVGGEGGASGRSP

Important features:

Signal peptide:

amino acids 1-18

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FIGURE 501

CAGGAGAGAAGGCACCGCCCCACCCCGCCTCCAAAGCTAACCCCTCGGGCTTGAGGGGAAGAG
GCTGACTGTACGTTCCCTTCTACTCTGGCACCCTCTCCAGGCTGCCATGGGGCCCAGCACCCC
TCTCCTCATCTTGTTCCCTTTTGTCATGGTCGGGACCCCTCCAAGGACAGCAGCACCACCTTGT
GGAGTACATGGAACGCCGACTAGCTGCTTTAGAGGAACGGCTGGCCCAGTGCCAGGACCAGAG
TAGTCGGCATGCTGCTGAGCTGCGGGACTTCAAGAACAAGATGCTGCCACTGCTGGAGGTGGC
AGAGAAGGAGCGGGAGGCACTCAGAACTGAGGCCGACACCATCTCCGGGAGAGTGGATCGTCT
GGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTCTGCCCTGTGTAGAGTTTGATGA
GAAGGTGACTGGAGGCCCTGGGACCAAAGGCAAGGGAAGAAGGAATGAGAAGTACGATATGGT
GACAGACTGTGGCTACACAATCTCTCAAGTGAGATCAATGAAGATTCTGAAGCGATTTGGTGG
CCCAGCTGGTCTATGGACCAAGGATCCACTGGGGCAAACAGAGAAGATCTACGTGTTAGATGG
GACACAGAATGACACAGCCTTTGTCTTCCCAAGGCTGCGTGACTTCACCCTTGCCATGGCTGC
CCGGAAAGCTTCCCGAGTCCGGGTGCCCTTCCCCTGGGTAGGCACAGGGCAGCTGGTATATGG
TGGCTTTCTTTATTTTGCTCGGAGGCCTCCTGGAAGACCTGGTGGAGGTGGTGAGATGGAGAA
CACTTTGCAGCTAATCAAATTCCACCTGGCAAACCGAACAGTGGTGGACAGCTCAGTATTCCC
AGCAGAGGGGGCTGATCCCCCCTACGGCTTGACAGCAGACACCTACATCGACCTGGTAGCTGA
TGAGGAAGGTCTTTGGGCTGTCTATGCCACCCGGGAGGATGACAGGCACTTGTGTCTGGCCAA
GTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGGACACACCATGTCCCAGAGAGAATGC
TGAGGCTGCCTTTGTCATCTGTGGGACCCTCTATGTCGTCTATAACACCCGTCTGCCAGTCG
GGCCCGCATCCAGTGCTCCTTTGATGCCAGCGGCACCCTGACCCCTGAACGGGCAGCACTCCC
TTATTTTCCCCGCAGATATGGTGCCCATGCCAGCCTCCGCTATAACCCCCGAGAACGCCAGCT
CTATGCCTGGGATGATGGCTACCAGATTGTCTATAAGCTGGAGATGAGGAAGAAAGAGGAGGA
GGTTTTGAGGAGCTAGCCTTGTTTTTTGCATCTTTCTCACTCCCATACATTTATATTATATCCC
CACTAAATTTCTTGTTCCCTCATTCTTCAAATGTGGGCCAGTTGTGGCTCAAATCCTCTATATT
TTTAGCCAATGGCAATCAAATCTTTTCACTCCTTTGTTTCATACGGAACTCCAGATCCTGAG
TAATCCTTTTAGAGCCCGAAGAGTCAAAACCCTCAATGTTCCCTCCTGCTCTCCTGCCCATG
TCAACAAATTTTCAAGGCTAAGGATGCCCCAGACCCAGGGCTCTAACCTTGTATGCGGGCAGGCC
CAGGGAGCAGGCAGCAGTGTTCTTCCCCTCAGAGTGAAGTGGGGAGGGAGAAATAGGAGGAGA
CGTCCAGCTCTGTCCTCTCTTCCCTCACTCCTCCCTTCAGTGTCCTGAGGAACAGGACTTTCTC
CACATTGTTTTGTATTGCAACATTTTGCATTAAAGGAAAATCCACAAAAA
AAA

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FIGURE 502

MGPSTPLLLILFLLSWGPLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKML
PLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGRRN
EKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRLRDF
TLAMAARKASRVRVFPWPVGTGQLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLANRTVV
DSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTQQWDTP
CPRENAEAAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAHASLRYN
PRERQLYAWDDGYQIVYKLEMRKKEEV

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

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FIGURE 503

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGGT
CTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGGCC
CTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAAGAA
CGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTCAGCA
CGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAACTCCGGATGGGTGTT
TGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGACTATGC
CATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGTACAGTCT
GACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGCCTGGGCTT
CCTGTCACAGTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGATCCTTCTGTG
AGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCAGTGTCCACCC
ACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATTCCACAGCA

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FIGURE 504

MGGLLLAFLALVSVPRQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVTL
TPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIIFTQLEF
GDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Important features:

Signal peptide:

amino acids 1-20

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FIGURE 505

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCACA
GCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAATC
CTGCTTGCTCTGGCAACAGGGCTTGAGGGGGAGAGACCAGGATCATCAAGGGGTTTCGAGTGC
AAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGGGGCG
ACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACATAGTT
CACCTGGGGCAGCACAACCTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCCACTGAG
TCCTTCCCCCACCCTGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGACATCATG
CTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCTCTCCTCA
CGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCCAGCCCCAG
TTACGCCTGCCTCACACCTTGCGATGCGCCAAACATCACCATCATTGAGCACCAGAAGTGTGAG
AACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGGAAGGGGGCAAG
GACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTTCAAGGCATTATC
TCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAA
TATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCACCCACCACAGCCCA
TCACCCTCCATTTCCACTTGGTGTGTTGGTTCCTGTTCACTCTGTTAATAAGAAACCCTAAGCC
AAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATGCTGTCACTTAATAATC
AACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTTGAAATATTGTGACTCTG
GGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCAAAGACAGCTCCTGGCCAT
ATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAA

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FIGURE 506

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHC
LKPRYIVHLGQHNLOKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITWAV
RPLTLSSRCVTAGTSC LISGWGSTSSPQLRLPHTLR CANITII EHQKCENAYPGNITDTMVCA
SVQEGGKDSCQGD SGGPLVCNQSLQGIISWGQDPCA ITRKPGVYTKVCKYVDWIQETMKNN

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

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FIGURE 507

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGACATGAGG
AGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAGCA
CCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAGGCC
TGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGCTGTTCCCTGTC
CAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCATCCTT
CCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCCTGAGTCCCGAGCCC
GACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGGCCCCGGTTG
TGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACATCTACCAC
CCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCCGCCCTGTCCCAAGGCCCAGGCTGTTGGGA
CTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAAAAAAAAAAAA
AAAAAA

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FIGURE 508

MRRLLLVTSLVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
F
PVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEERP
RLWVMPNHQVLLGPEEDQDHIYHPQ

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FIGURE 509

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCCC
ACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCGCG
CTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCCATG
GCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAACAGAG
ACTCTCCAACATGTGCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAACCACCA
ACTTCAGTTGCCTCAGACTCCAGTAATAACAACGGTCACCACCATGAAACCTACAGCGGCATCT
AATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTCTACACCC
AAAACAACAAGTGTTTCACAGAACACATCTCAGATATCAACATCCACAATGACCGTAACCCAC
AATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCATTCTGAAGCA
AAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAACGCTGGGAGTT
TTATCTATTCTTTACATTGGATGCAAATGTATTACTCAAGAAGAGGCATTTCGGTATCGAACC
ATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGAATACAGATTGAT
GCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAACAATATTCTCTTTTTTGAAAATA
GTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTAAAGATTCTTCAAGG
TAACAAGGGTTTGGGTTTTTGAAATAAACATCTGGATCTTATAGACCGTTCATACAATGGTTTT
AGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTTGGCTGGGGTGGGGGCATTGG
TCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAATGCCATCTGGGCATACA
AATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGTAGCTCACATAAAGAACTT
CAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACACAGAAATTATACAATCAAA
CTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTGTGCTTTAACTGTAGTAGTT
GGTCTAGAAACAAAATACTCC

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FIGURE 510

MGLGARGAWAALLLGTLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPDHT
NETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQNTS
QISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIGCKM
YYSRRGIRYRTIDEHDAII.

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FIGURE 511

GACTTTGCTTGAATGTTTACATTTTCTGCTCGCTGTCCTACATATCACAATATAGTGTTACGTTTTGTAAAAC
TTTGGGGTGTGAGGAGTTGAGCTTGCTCAGCAAGCCAGCATGGCTAGGATGAGCTTTGTTATAGCAGCTTGCCAA
TTGGTGCTGGGCCTACTAATGACTTCATTAACCGAGTCTTCCATACAGAATAGTGAGTGTCACAACCTTTGCGTA
TGTGAAATTCGTCCCTGGTTTACCCACAGTCACTTACAGAGAAGCCACCAGTGTGATTGCAATGACCTCCGC
TTAACAAGGATTCCAGTAACCTCTCTAGTGACACACAAGTGCTTCTCTTACAGAGCAATAACATCGCGAAGACT
GTGGATGAGCTGCAGCAGCTTTTCAACTTGACTGAAGTAGATTTCTCCCAAAACAACCTTTACTAACATTAAGGAG
GTCGGGCTGGCAAACCTAACCCAGCTCACAACGCTGCATTTGGAGGAAAATCAGATTACCGAGATGACTGATTAC
TGTCTACAAGACCTCAGCAACCTTCAAGAACTCTACATCAACCACAACCAAAATTAGCACTATTTCTGCTCATGCT
TTTGCAGGCTTAAAAAATCTATTAAGGCTCCACCTGAAGTCCAACAAATTGAAAGTTATTGATAGTCGCTGGTTT
GATTCTACACCCAACCTGGAAATTCTCATGATCGGAGAAAACCTGTGATTGGAATTCTGGATATGAAGTTCAAA
CCCCTCGCAAATTTGAGAAGCTTAGTTTTGGCAGGAATGTATCTCACTGATATTCCTGGAAATGCTTTGGTGGGT
CTGGATAGCCTTGAGAGCCTGTCTTTTTATGATAACAACTGGTTAAAGTCCCTCAACTTGCCCTGCAAAAAGTT
CCAAATTTGAAATTCCTTAGACCTCAACAAAAACCCATTCAACAAATCCAAGAAGGGGACTTCAAAAATATGCTT
CGGTTAAAAGAACTGGGAATCAACAATATGGGCGAGCTCGTTTCTGTGCGACCGCTATGCCCTGGATAACTTGCCT
GAAGTCAACAAAGCTGGAAGCCACCAATAACCTAACTCTCTTACATCCACCGCTTGGCTTTCCGAAGTGTCCCT
GCTCTGGAAGCTTGATGCTGAACAACAATGCCTTGAATGCCATTTACCAAAAAGACAGTCGAATCCCTCCCAAT
CTGCGTGAGATCAGTATCCATAGCAATCCCCTCAGGTGTGACTGTGTGATCCACTGGATTAAGTCCAACAAAACC
AACATCCGCTTCATGGAGCCCCTGTCCATGTTCTGTGCCATGCCGCCGAATATAAAGGGCACCAGGTGAAGGAA
GTTTTAATCCAGGATTCGAGTGAACAGTGCCTCCCAATGATATCTCACGACAGCTTCCCAATCGTTTTAAACGTG
GATATCGGCACGACGGTTTTCTTAGACTGTGCGAGCCATGGCTGAGCCAGAACCTGAAATTTACTGGGTCACTCCC
ATTGGAATAAGATAACTGTGGAACCCCTTTCAGATAAATACAAGCTAAGTAGCGAAGGTACCTTGGAATATCT
AACATACAAATTGAAGACTCAGGAAGATACACATGTGTTGCCAGAATGTCCAAGGGGCAGACACTCGGGTGGCA
ACAATTAAGGTTAACGGGACCCCTTCTGGATGGTACCCAGGTGCTAAAAATATACGTCAAGCAGACAGAATCCCAT
TCCATCTTAGTGTCTGGAAGTTAATTCATGTGACGTCAAAGTAAAATGGTCGTCTGCCACCATGAAG
ATTGATAACCCCTCACATAACATATACTGCCAGGGTCCCAGTCGATGTCCATGAATACAACCTAACGCATCTGCAG
CCTTCCACAGATTATGAAGTGTGTCTCACAGTGTCCAATATTCATCAGCAGACTCAAAGTCAATGCGTAAATGTC
ACAACCAAAAATGCCGCCTTCGCAGTGGACATCTCTGATCAAGAAACCACTACAGCCCTTGCTGCAGTAATGGGG
TCTATGTTTGCCGTATTAGCCTTGCGTCCATTGCTGTGTACTTTGCCAAAAGATTTAAGAGAAAAAACTACCAC
CACTCATTAATAAAGTATATGCAAAAAACCTCTTCAATCCCACTAAATGAGCTGTACCCACCACTCATTAACCTC
TGGAAGGTGACAGCGAGAAAGACAAAGATGGTTCTGCAGACACCAAGCCAACCCAGGTGACACATCCAGAAGC
TATTACATGTGGTAACTCAGAGGATATTTTGCTTCTGGTAGTAAGGAGCACAAAGACGTTTTTTGCTTTATTCTGC
AAAAGTGAACAAGTTGAAGACTTTTGTATTTTGAAGTTTGTAGTTTGTGGCAGAGTGGAGAGGACGGGTGGATA
TTTCAAATTTTTTTTAGTATAGCGTATCGCAAGGGTTTGACACGGCTGCCAGCGACTCTAGGCTTCCAGTCTGTGT
TTGGTTTTTTATTCTTATCATTATTATGATTGTTATTATATTATTTATTTTAGTTGTTGTGCTAAACTCAAT
AATGCTGTTCTAACTACAGTGCTCAATAAAATGATTAATGACAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

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FIGURE 512

MARMSFVIAACQLVLGLLMTSLTESSIONSECPQLCVCEIRPWFTPQSTYREATTVDCNDLRL
TRIPSNLSSDTQVLLLQSNNIAKTVDELQQLFNLTELDIFSQNNFTNIKEVGLANLTQLTTLHL
EENQITEMTDYCLQDLSNLQELYINHNIQISTISAHAFAGLKNLLRLHLNSNKLKVIDSRWFDS
TPNLEILMIGENPVIGILDMNFKPLANLRSLVLAGMYLTDIPGNALVGLDSLESLSFYDNKLV
KVPQLALQKVPNLKFLDLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSVDRYALDNLPELT
KLEATNNPKLSYIHLAFRSVPALESMLNNNALNAIYQKTVESLPNLREISIHNSNPLRCDCV
IHWINSNKTNI RFMEPLSMFCAMPPEYKGHQVKEVLIQDSSEQCLPMISHDSFPNRLNVDIGT
TVFLDCRAMAEPEPEIYWVTPIGNKITVETLSDKYKLSSEGTLEISNIQIEDSGRYTCVAQNV
QGADTRVATIKVNGTLLDGTQVLKIYVKQTESHSILVSWKVN SNVMTSNLKWSSATMKIDNPH
ITYTARVPVDVHEYNLTHLQ PSTDYEVCLTVSNIHQQTQKSCVNVTTKNAAFVAVDISDQETST
ALAAVMGSMFAVISLASIAVYFAKRFRKKNYHSLKKYMQKTSSIPLNELYPPLINLWEGDSE
KDKDGSADTKPTQVDTSRSYMW

Important features:**Signal peptide:**

Amino acids 1-25

Transmembrane domain:

Amino acids 508-530

N-glycosylation sites:Amino acids 69-73;96-100;106-110;117-121;385-389;517-521;
582-586;611-615**Tyrosine kinase phosphorylation site:**

Amino acids 573-582

N-myristoylation sites:

Amino acids 16-22;224-230;464-470;637-643;698-704

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FIGURE 513

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC
CAGCAATATGCATCTTGACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT
GTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT
GAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGCATGC
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT
GGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAATGC
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGCAACCATCAAAG
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA
CACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCTTAAACTGG
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGACATGACCTGGAGGGG
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTGTACTGGGATTTGTGAATAAA
CTTGATACACCA

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FIGURE 514

MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAGR
EVEKVFNGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAGQA
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

Important features:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

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FIGURE 515

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCTT
TTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCGAA
CCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCGGAG
AAGCGGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTTGGGG
CCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCGGTGTG
CGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGGTTCGCCG
GCCGGCCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCGCCGCTGCTACCCCTGCGCCCCG
TGCGAGCCCCGGCGTCCGGCCCCGCGCCCTGCGCTCATGGACGGCGGGCTCCCGGCTGGCGGGCGG
CGCCCCCGGGCTGTGAATGCGACTCGCCCCCTCGGCCGCGCTCCCCGCCCCGCCCCGCCGG
GACGTGGTAGGGGATGCCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCAGTTCCCTCCT
GGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAGAAGCTGGCCCA
GGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGGCCCGGGGCGGGT
GAACGAGCTCGGGCGCCCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACTGGAAGAGCAAGAG
CGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCCTGGGTCTCCCAGGG
CGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGGACACCCCGCAGGCGGAAGC
CCTGGCCGCAGCCGCCCAGGACGCGATTGGCCCGGAACCTCGCGCCCACGCCCGAGCCACCCGA
GGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAGAGCGGCTTCGTGTACGC
GATCGGGGAGAAGTTCGCGCCGGGCCCCCTCGGCCTGCCCGTGCCTGTGCACCGAGGAGGGGCC
GCTGTGCGCGCAGCCCGAGTGCCCGAGGCTGCACCCGCGCTGCATCCACGTCGACACGAGCCA
GTGCTGCCCCGAGTGCAAGGAGAGGAAGAACTACTGCGAGTTCCGGGGCAAGACCTATCAGAC
TTTGGAGGAGTTTCGTGGTGTCTCCATGCGAGAGGTGTGCTGTGAAGCCAACGGTGAGGTGCT
ATGCACAGTGTGAGCGTGTCCCCAGACGGAGTGTGTGGACCCTGTGTACGAGCCTGATCAGTG
CTGTCCCATCTGCAAAAATGGTCCAAACTGCTTTGCAGAAACCGCGGTGATCCCTGCTGGCAG
AGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTACTTATGAGGAAGGCACATGGAGAAT
CGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGCAAATGTAGACGCTTCCCAGAACACA
AACTCTGACTTTTTTCTAGAACATTTTACTGATGTGAACATTCTAGATGACTCTGGGAACTATC
AGTCAAAGAAGACTTTTGTATGAGGAATAATGGAAAATTGTTGGTACTTTTCCTTTTCTTGATA
ACAGTTACTACAACAGAAGGAAATGGATATATTTCAAACATCAACAAGAACTTTGGGCATAA
AATCCTTCTCTAAATAAATGTGCTATTTTCACAGTAAGTACACAAAAGTACACTATTATATAT
CAAATGTATTTCTATAATCCCTCCATTAGAGAGCTTATATAAGTGTTTTCTATAGATGCAGAT
TAAAAATGCTGTGTGTGTCAACCGTCAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 516

MPSSTAMAVGALSSSLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNELG
RPARDEGGSGRDWKS KSGRGLAGREPWSK LKQAWVSQGGGAKAGDLQVRPRGDT PQAEALAAA
AQDAIGPELAPTPEPPEEYVYPDYRGKGCVD ESGFVYAIG EKFA PGPSAC PCLCTEEGPLCAQ
PECPRLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRC EANGEVLCTVS
ACPQTECVDPVYEPDQCCPICKNGPNCFAETA V I PAGREVKTDECTICHCTYE EGTWRIERQA
MCTRHECRQM

Important features:**Signal peptide:**

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

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FIGURE 517

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCCT
TTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCTAC
GGACGACGCCTATGAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTGTGC
CGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATACAAG
TTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAAATCTAACT
CTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTACACATG
GAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACAACCTTTCC
CTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCCATTTCTGGT
CGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTGAAAATGAAG
AGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATGTTGCCAGTTG
TACTGAATCATCTACAAGTCCATATGTTACCTCATAACAAGTCACCTGTCACCACTTTAGATA
AGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCTCAGGTGAACTG
CGATAGAAAAACCCGAAGAGTTTGAAAGCACCCAGAGAGTTGGAATAATGATGACATTTTGA
AAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGACACCAGCAACCCAG
CATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCCTTGCTCTAGCAGCAG
CAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCAGTAGGACGAACAAGTA
ATAAAATTGATGACATCGAAACTGTTATTAACATGCTGTGTAATTCTAGATCTAACTCTATG
AATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAGCTGCTACAGTATTCAATA
CATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTAAAAGTTTATTAAACAATAA
TATAAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGATTTAAGCAAACCTGCATTTTT
TCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTATAAAAATATTTTCTATTGTAGT
TCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACAATTTTCATATGCACTAAAAACC
TAATTTAAAATAAAATTTTGGTTCAGGAAAAAA

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FIGURE 518

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVSPSGEPGREKKSNSPKH
VYSIASKGSKFKELVTHGDASTENDVLNPISEETTTFTPTGGFTPEIGKKKHTESTPFWSIKP
NNVSIVLHAEOPYIENEEPEPEPEPAAKQTEAPRMLPVVTESSSTSPYVTSYKSPVTTLDKSTG
IEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNPAYRE
DIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKLYEYLD
IKCVPPREMREKAATVFNTLKNMCRSRRVTALLKVY

Important features:**Signal peptide:**

amino acids 1-19

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FIGURE 519

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTTG
GATTTGAAAGTTGAGAGCAGC**ATG**TTTTTGCCCACTGAAACTCATCCTGCTGCCAGTGTTACTG
GATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTGGGT
GATTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGATAGAC
TGGACTCTGTCAACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCAATCTC
AGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGGGACATCTTATGCAATGAT
GGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCGC
CTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAGAGGAGCCC
AAAGAGCTCATGGTCCATGTGGGTGGATTGATTCAGATGGGATGTGTTTTCCAGAGCACAGAA
GTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGAGGAGATTGTA
TTTCGTTACTACCACAAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGGGCCACTTCCAG
AATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCATCATGCTTCAAGGAGTG
AGGGAGTCAGATGGAGGAAACTACACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAGAAA
ACCATTGTGCTGCATGTCAGCCCCGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGG
CCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTG
CTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAGTGAATTCT
ACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCCTGCCATTTT
GAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAA
GAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCTTCTCTG
AGGTCAGATCGGAACAACTCACTTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA
GCCTTTT**TGA**GAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTGTGT
GTCCTGGGCCACTCTACCAGTGATTTTCAGACTCCCGCTCTCCAGCTGTCCTCCTGTCTCATT
GTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGGCAGAGAGACTGGACAGCTCTGGA
GGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTGGCCCTG
GGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCCGTTGGATCAGACCCTCCTGTGGGCAGGG
TTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAACCAACCCAAATCAA

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FIGURE 520

MFCPLKLILLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS PGE
HAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLKGESQV
FKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKL
RMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIVLHVS
PEEPRTLVT PAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKT CGNKSSVNSTVLVKNT
KKTNP EIKEKPCHFERCEGEKHIYSP IIVREVIEEEEPSEKSEATYMTMHPVWPSLRSDRNNNS
LEKKSGGGMPKTQQAF

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FIGURE 521

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATGG
TTCTACCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGGAA
ACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGGCCATGCAGGA
TGAAGATGGATACATCACCTTAAATATTA AAACTCGGAAACCAGCTCTCGTCTCCGTTGGCCC
TGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGGATGGT
TGTCGGGCTGGTGGCTCTGGGGATTTGGTCTGTCATGCAGCGCAATTACCTACAAGATGAGAA
TGAAAATCGCACAGGA ACTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGGTAAAACA
ATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCCTGTGACACAACTGGAGATA
TTATGGAGATAGCTGCTATGGGTCTTCAGGCACAACTTAACATGGGAAGAGAGTAAGCAGTA
CTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGGAGTACATCAA
AGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAATGAGGTCTGGAA
GTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGAAGATGGAAAAGGAAA
TATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTGAGAACAAACATTA
TTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCTTAATGCAAAGAGGT
GGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGTATGAATGCATCAGTA
GCTGAAAAAAAAAAAAA

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FIGURE 522

MQDEDGYITLNIKTRKPALVSVGPASSSWWRVMALILLILCVGMVVGLVALGIW\$VMQARNYLQ
DENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYG\$SCYGFFRHNL\$TWEES
KQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDG
KGNMNCAYFHNGKMHPTFCENKH\$YLMCERKAGMTKVDQLP

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FIGURE 523

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGC
AAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAA
GAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCTAAT
TGTCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGA
GCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAG
AACTGAAATATTGAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAA
CGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGT
GATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTT
CTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAA
AAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATCCCCTCTAAT
ATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTTCCTGCCAACGA
AAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCG
TCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTGAAAATGGAATAGA
ATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTA
TTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATACTGCTACCAAGGAGG
ACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCCGCATGCTGGGGAGGGT
CTAATAGGAGGTTTGAGCTCAAATGCTTAACTGCTGGCAACATATAATAAATGCATGCTATT
CAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCTCTCCAGAATTACTTGTAG
GTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 524

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYD
MEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIYFVGLQKCFIKTQI
KVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKN SKILEICDNVTMYWINPT
LISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENG
IEFDPMLDERGYCCIIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

Important features:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

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FIGURE 525

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAAGATCACTGGGGGTC
TCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCCAA
AAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCACAT
ACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACCTTGTGTACCGAGA
GCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTTAAATTCTCCATGGAC
ATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTGAGTTTC
TTTCAGTTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTGACTGAAT
GGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCATTTTTTTTTT
TAACACGTCAATAAAAAAATAATCTCCAGA

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FIGURE 526

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGNE
CHLCTESLKSNQGRVQFLHDGSC

Important features:

Signal peptide:

amino acids 1-19

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FIGURE 527

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTGG
CTGCGGCGCTGCTCTCGTCGCTTGCGCGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGGCCT
CGTCGCTCAGCCCCCTATTTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTATTGT
CGGGCCCCGAGGCTCCGTGGCGGGACCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTGCAGC
TGGTCGCCCCTCATTCGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCTGAGGC
AGCTGCACGGGTTGCTGCAGGCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTACCGGCAGCC
GCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGACGGGCAGC
TAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCTCTTCCCGG
CCCTTTTTCAGCCGTGAGAACTACGGCCGCCTGCGGCTCATCACCAGTTCCAAGCACCGCTGCA
TGGATAGCAGCGCCGCCTTCTTGCAGGGGCTGTGGCAGCACTACCACCCTGGCTTGCCGCCGC
CGGACGTGCGCAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAATGAGATTTTTTG
ATCACTGTGAGAAGTTTTTAAGTAGAAAAAATGCTACAGCTCTTTATCACGTGGAAG
CCTTCAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCTACTTTGCAAGTGC
CAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTCACCTGTTTCAATTTGACCTGG
CAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTTGACATAGATGATGCAAAGGTATTAG
AATATTTAAATGATCTGAAACAATATTGGAAAAGAGGATATGGGTATACTATTAACAGTCGAT
CCAGCTGCACCTTGTTTCAGGATATCTTTCAGCACTTGGACAAAGCAGTTGAACAGAAACAAA
GGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATGCAGAGACTCTTCTTCCAC
TGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACAGCGTACAATTACAAAAAAC
AAATGCATCGGAAGTTCCGAAGTGGTCTCATTGTACCTTATGCCTCGAACCTGATATTTGTGC
TTTACCCTGTGAAAATGCTAAGACTCCTAAAGAACAAATCCGAGTGCAGATGTTATTAATG
AAAAGGTGTTACCTTTGGCTTACTCACAAGAACTGTTTCATTTTATGAAGATCTGAAGAACC
ACTACAAGGACATCCTTCAGAGTTGTCAAACCAGTGAAGAATGTGAATTAGCAAGGGCTAACA
GTACATCTGATGAACTATGAGTAACTGAAGAACATTTTTAATTCTTTAGGAATCTGCAATGAG
TGATTACATGCTTGTAATAGGTAGGCAATTCCTTGATTACAGGAAGCTTTTATATTACTTGAG
TATTTCTGTCTTTTCACAGAAAAACATTGGGTTTCTCTCTGGGTTTGGACATGAAATGTAAGA
AAAGATTTTTTCACTGGAGCAGCTCTCTTAAGGAGAAACAAATCTATTTAGAGAAACAGCTGGC
CCTGCAAATGTTTACAGAAATGAAATTCCTTCTACTTATATAAGAAATCTCACACTGAGATAG
AATTGTGATTTTACATAATAACACTTGAAAAGTGCTGGAGTAACAAAATATCTCAGTTGGACCAT
CCTTAACCTGATTGAACTGTCTAGGAACCTTACAGATTGTTCTGCAGTTCTCTCTTCTTTCC
TCAGGTAGGACAGCTCTAGCATTTTCTTAATCAGGAATATTGTGGTAAGCTGGGAGTATCACT
CTGGAAGAAAGTAACATCTCCAGATGAGAATTTGAAACAAGAAACAGAGTGTGTAAAAGGAC
ACCTTCACTGAAGCAAGTCGGAAAGTACAATGAAAATAAATATTTTTGGTATTTATTTATGAA
ATATTTGAACATTTTTTCAATAATTCCTTTTTACTTCTAGGAAGTCTCAAAGACCATCTTAA
ATTATTATATGTTTGGACAATTAGCAACAAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCC
ATTGCTTAGCTAACTTTTTTCATTCTGTCACTTGGCTTCGATTTTTATATTTTCTATTATATG
AAATGTATCTTTTGGTTGTTTGATTTTTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCA
AATGCCGTGAAAGTATTTGCTATAATAAGAAAATTCCTTGTGACTTTAAAAA

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FIGURE 528

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPLYFGTKTRYEDVNPVLLSG
PEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGSRD
LGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHRCMD
SSAAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYHVEAF
KTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSEFDLAIKGVKSPWCDVFDIDDAKVLEY
LNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAETLLPLL
SLMGYFKDKEPLTAYNYKKQMHRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRVQMLLNEK
VLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

Important features:**Signal sequence**

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

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FIGURE 529

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTGG
CGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGGGA
CGCGGCGGCGGGCGGCGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGGAGCCGGGGCG
GTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGCTGGCGGCGGCGCTTGGGCTC
TTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAAATGGT
ACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTC
TCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTGCTTTTTTCCACTACTCCCAAGGG
CAAGTGTACCTTGGGAATTATCCACCATTTAAAGACAGAATCAGCTGGGCTGGAGACCTTGAC
AAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACCTATATCTGT
GATGTCAAAAACCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTATGTCGTAGAA
AAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTGCTGTGGTCCTA
GGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCTCTATAGAAGGAAAACTCTAAACGG
GATTACACTGGCTGCAGTACATCAGAGAGTTTGTACCAGTTAAGCAGGCTCCTCGGAAGTCC
CCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACCAGGGCCAGTCATA
TATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAACAAGTCAGAGTCTGTG
GTGTATGCGGATATCCGAAAGAATTAAAGAGAATACCTAGAACATATCCTCAGCAAGAAACAAA
ACCAAACCTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGTAGCCTTGGAGACCCAGG
CAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGTACAAAGGATATGTATAAA
TATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGATGAAAAGATGGTATGATTC
TACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTCAGGTCATTTACAATTGGGAG
ATTTTCAGAAACATTCCTTTTACCATCATTTAGAAATGGTTTGCCTTAATGGAGACAATAGCAG
ATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAGGGCTTAAGACTGATTAGTCTTA
GCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAAGCATACCCAGGGTGGCCTTTAGC
ACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAAAATACCCATTGGCTATGCCACTTG
AAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACTAAAATATGGGGCAATTGTTAGCCTT
ACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTGAAATGTGTATATCAATTTCTGGATT
CATAATAGCAAGATTAGCAAAGGATAAATGCCGAAGGTCATTCTTGACACAGTTGGAT
CAATACTGATTAAGTAGAAAATCCAAGCTTTGCTTGAGAACTTTTGTAACTGGAGAGTAAAA
AGTATCGGTTTTTA

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FIGURE 530

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKST
STTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKKDASINIENMQ
FIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMILAV
LYRRKNSKRDTGCTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSGGHHS
DKINKSESVVYADIRKN

Important features:**Signal peptide:**

amino acids 1-37

Transmembrane domain:

amino acids 161-183

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FIGURE 531

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCGA
GGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGCTC
TTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCGGGGCAGCGGCTGCCGGGCCGGGACTGGT
GCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCTGCTG
GAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCTGGAAC
CAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGGAGCGGGGCCGACTC
CGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGGGGCCCTG
GATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGGTGGAGTCG
CACCTGTCGGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGCGTGTGCGTG
GTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGAGCTGTTCAAC
ACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGGCCTTCATTGAG
CGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAGTCCTTCTTCGCC
AAATACTGGATGTACATCATTTCCCGTCGTCCTGTTCCCTCATGATGTCAGGAGCGCCAGACACC
GGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCCTTTGCTGTGTGCCA
CCCTCCCTGTAAGTCTATTTAAAAACATCGACGATACATTGAAATGTGTGAACGTTTTGAAAA
GCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGGTCCTGATGTACAAGCT
TGATTGAAATTCAGTCTCACTTGATACGTTATTAGAAACCCAAGGAATGGCTGTCCCCATC
CTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTATTAAACTGTCCCCAGATC
GACACGCAAAAAAAAAA

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FIGURE 532

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEID
DSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIPRRPGALDGLEAGG
YVSSFVPACSLVESHLSQDLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQLQP
PTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWMYIIPVVLFLMMSGAPDTGGQGGGG
GGGGGGGSGLCVPPSL

Important features:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 226-243

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FIGURE 533

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTGAT
GGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGAC
TGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGG
CCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACCTGAA
GACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCATACATTGTATGGATTTATC
TCAACGCTATTGTTTAATGGCTGTGTTTAATGTGATCTATCTGGAAAATGAGGACTCCGAATA
AAAAGCTATTACTAWTTNAAA
AAA

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FIGURE 534

MELALLCGLVVMAGVPIPIQGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWC
CQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDL SQRYCLMAVFNVIIYLENEDSE

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

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FIGURE 535

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTG
AACTGGGTGCTCATCACGGGAAGTGTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCC
CCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTT
TTTTTAACCGCCCCCTCCCCACCCCCCAAAAACTGTAAAGATGCAAAAACGTAATATCCAT
GAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTT
GTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAG
GGGTCCAATTTTTCTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGG
CTGTCATGCAACTGGCCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAACAATACAA
AGGATGGGTTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCC
ACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAA
GGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTATATCTGCTGGT
TGCTTAGGTTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTTAAGTATAATCAATTTAAAGGG
CTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATATTGACGAAAATGCT
TTAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAATCTCCTATTTTTCTT
AACAATACCTTCAGACCTGTGACAAATTTACGGAACTTGGATCTGTCTTATAATCAGCTGCAT
TCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTTACATTTACGGTCTAAC
TCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACCTGGAACCTTTTGGACCTG
GGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGCATGATCAGACTCAAAGAA
CTTCACCTGGAGCACAAATCAATTTTCCAAGCTCAACCTGGCCCTTTTTCCAAGGTTGGTCAGC
CTTCAGAACCTTTACTTGCAGTGGAAATAAAATCAGTGTCAATAGGACAGACCATGTCTGGACC
TGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATCGAAGCTTTCAGTGGACCCAGT
GTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGATTCCAACAAGCTCACATTTATT
GGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAGTCTTGCTGGGAATATATGG
GAATGCAGCAGAAATATTTGCTCCCTTGTAACCTGGCTGAAAAGTTTTAAAGGTCTAAGGGAG
AATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTGATCGATGCAGTGAAG
AACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAGGGCTCTCCCAAAG
CCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAACCCCTTTGCCCCCGACG
GTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTTTCCATAAA
ATCATCGCGGGCAGCGTGGCGCTTTTCCTGTCCGTGCTCGTCATCCTGCTGGTTATCTACGTG
TCATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAAGGCAC
AGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCCAGCACCCAGGAATTTTATGTAGAT
TATAAACCCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCCTGCACCTAT
AACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTTGTGATAAAAAGAGCTCTTAAAGC
TGGGAAATAAGTGGTGCTTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCCTC
CCCTTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCCTTGTCGGTTTTAGTGCATTCATA
ATACTGGTCATTTTCCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGT
GAAGCTTGAACCTCCGGTTTAATATAATACCTATTGTATAAGACCCTTACTGATTCCATTAAT
GTCGCATTTGTTTTAAGATAAAACTTCTTTCATAGGTAAAAA

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FIGURE 536

MGFNVIRLLSGSAVALVIAPTIVLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGC
LGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYFLN
NTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRI FQDCRNLELLDLG
YNRIRSLARNVFAGMIRLKEHLHLEHNQFSKLNALFPRLVSLQONLYLQWNKISVIGQTMSWTW
SSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLD SNKLTFIGQEILDSWISLNDISLAGNIWE
CSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKP
TFKPKLPRPKHESKPPLPPTVGATEPGPETDADAHEHISFHKIAGSVALEFLSVLVILLVIYVS
WKRYPASMKQLQQRSLMRRHRKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLNGTGPCTYN
KSGSRECEV

Important features:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

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FIGURE 537

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAAGTGTCTTGATCATTACGGATTTCGC
AGACAAGTGACCCAGGATCGAGTGAAGAAAATTCAGATGAACAAACACATATGTGTTTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCCTACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCCAGATTTTCGAATTCTTCTTTCCACTTAAACTCTGAAACAGGCACCTTGGTGTTCACCTGCTG
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGGTTGTCCTTGCTGTACTGGCCCTGA
TCAGTTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAACACAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTTCAGAAAGCTTTTCGTTTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCCTCAAGATGGACCCGGTAAATATAACCAAA
GGAAGCGAAACTGGGTGCGTTCAGTGAGTTGGGTTCCTAATCTGTTTCTGGCCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTTGCTCACGTAAACGCCCGTGTGGGCCCTGTGAAGCCAGCATGTTTACCAGTGGTTCGTT
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGGGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGAGTTTCTTCTTAAAGGCTCTGC
TGATCGGTGTTGCAAGTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG
GTAAATTGGTTGCTGGAAGAGGGATCTTGCTGAGGAACCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTATTTTATAAAATTT
TACATCTAAATTTTTGCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAACTGTAAATATATTGT
CATACAATGTTAAATAACCTATTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTTAAAT
TGAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTTCTTCT
CACACAAGTTTTAGCCTTTTTTACAAGGGAACCTACTACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAAATTCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAACAGACCTCT
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTTAAAGTTTGTATTAATTATTGTT
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT
CCCACTGTTCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTGAGGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAG
TGAAACGCCTGAATCAAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTCATCCGCCGGAGACACTGCTCCCATT
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCAGAAACCTT
GCCGTGCTGGACTCAGGACTGAAGTGCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCTGGA
GAATGGCTCTCACTACTACCTTGTCTTTTCAAGTGTCTTGGGTTTTTTTATACTTTGACAGCTTTTTTTT
AATGTCATACATGAGACTGTGTTGACTTTTTTTAGTTATGTGAAACACTTTGCCGCAGGCCGCTGGCAGAGGCA
GGAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACAGCTCCAGCCTCCT
TCTTGGTTGTATAGTGATAGGGTAGCCTTATTGCCCTCTCTTATACCTTAAACCTTCTACACTAGTGCCA
TGGAACACAGGTCTGAAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTTAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTGTGTTAAC
CTCATTTATAAAAGCTTCAAAAAACCCA

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FIGURE 538

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDF
RIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTS�KIWNVTRRDSALYRCEVVARNDRKEI
DEIVIELTVQVKPVTFCRVKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRANPR
FRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDLNIGGIIGGVLVV
LAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Important features:**Signal peptide:**

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

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FIGURE 539

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCTCAGAGGCCGGGGAAGAGAAGCAAAGC
GCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCTAA
CTTCAGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGG
CACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTCTGGGCAGCTGG
GCTCGGGCGGGCGGGAGTAGGGCCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTCGCGGG
CTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCGCCGGA
TGAGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCC
GCCGCGTGGTCAAGCGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGG
CCTACTTCCATGAAGTGTCCAGCCGAGTGAGCTTTTCAAGAGGCACGCCTGGCTTGTGAGAGTG
AGGGAGGAGTCCTCCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGC
AAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGAATTTCTGGATAGGGCTTTGGAGGA
ATGGAGATGGGCAAACATCTGGTGCCTGCCAGATCTCTACCAGTGGTCTGATGGAAGCAATT
CCCAGTACCGAACTGGTACACAGATGAACCTTCTGCGGAAGTGAAAAGTGTGTTGTGATGT
ATCACCAACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCAGTGAATGATGACA
GGTGTAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTAATCCAACAGCCCCTG
TAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAATGTGGTTGTTACTGAAG
CAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACCCCTGCTCTTACTGATAC
TGTTGCTTTTGGAACTGTTGTTTCCAGATGCTGCATAAAAGTAAAGGAAGAACAAAACTA
GTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAAGAAAGTGGCATGGAAGTAT
AATAACTCATTGACTTGGTTCCAGAATTTTGTAACTTCTGGATCTGTATAAGGAATGGCATCAG
AACAATAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGCAAGATGAAGTGAAGCTCCCCCT
TGAGGCAAATATTAAAGTAATTTTTATATGTCTATTATTTTCAATTTAAAGAATATGCTGTGCTA
ATAATGGAGTGAGACATGCTTATTTTGTAAAGGATGCACCCAACTTCAAACCTCAAGCAAA
TGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTATGTGTGTTAGAAGCAAT
TCCTTTTATTTCTTTTACCTTTTATAAGTTGTTATCTAGTCAATGTAATGTATATTGTATTGA
AATTTACAGTGTGCAAAAGTATTTTACCTTTGCTAAAGTGTGATAAAAATGAACTGTTCTA
ATATTTATTTTATGGCATCTCATTTTTCAATACATGCTCTTTTGATTAAAGAACTTATTAC
TGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGTCTTCTCGAA
ATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGAAATAAGA
AGCTATTTTCATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGATTGTCT
AATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTGTAGCTTAAAATTAAACAGATTTTG
TAATAATGTAACCTTGTAAATAGGTGCATAAAACACTAATGCAGTCAATTTGAACAAAAGAAGT
GACATACACAATATAAATCATATGTCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTG
AGGGTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTTCGGGGTTT
GGGATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGC
CTCTGACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAG
TGTGGAGACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACTACGAAATCGTGTGAAA
ATGGGTGGAACCCATCAGTGATCGCATATTCATTGATGAGGGTTTGTCTGAGATAGAAAATG
GTGGCTCCTTTCTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTCTTCTCAAGAGA
AAGTTGTAACCTCTGGTCTTCATATGTCCCTGTGCTCCTTTTAAACCAATAAAGAGTTCTTG
TTTCTGGGGGAAA

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FIGURE 540

MSRVVSLLLGAALLCGHGAFRRVVSQGKVCFADFKHPCYKMAYFHELSSRVSFQEARLACES
EGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSACPDLYQWSDGSN
SQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAP
VEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKGRTKT
SPNQSTLWISKSTRKESGMEV

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89 and 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145
and 212-217

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FIGURE 541

GGAGAATGGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCTGGTCCGGGGTGGTCTGTCTGCTCCTGGCATGCCCTG
CCACAGCCACTGGGCCCCGAAGTTGCTCAGCCTGAAGTAGACACCACCCTGGGTGCTGTGCGAGGCCGGCAGGTGG
GCGTGAAGGGCACAGACCGCCTTGTGAATGTCTTTCTGGGCATTCCATTTGCCAGCCGCCACTGGGCCCCGACC
GGTTCTCAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCCAATGTGCCTAC
AAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCTCAACGGAACAGCAGATCTTCTCCGTTTCAGAGGACT
GCCTGGTCTCAACGTCTATAGCCAGCTGAGGTCCCCGAGGGTCCGGTAGGCCGGTCATGGTATGGGTCCATG
GAGGCGCTCTGATAACTGGCGCTGCCACCTCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCTGG
TTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTCAGCACTGGAGATGAGCATGCACCTGGCAACCAGGGCT
TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCAACTGTGTCA
CTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCAGGGCTGTTCC
ACAGAGCCATCACACAGAGTGGGGTCACTACCACCCAGGGATCATCGACTCTCACCTTGGCCCCCTAGCTCAGA
AAATCGCAAAACACCTTGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAGCAGAAAGAAGGAG
AAGAGCTGGTCTTAGCAAGAAGCTGAAAAATACTATCTATCCTCTCACCGTTGATGGCACTGTCTTCCCCAAAA
GCCCCAAGGAACCTCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCTCATGGGTGTCAACAACCATGAGTGTCA
GCTGGCTCATCCCCAGGGGTGGGGTCTCTGGATACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCT
CAACACCCGTCTTGACCAGTCTGGATGTGCCCCCTGAGATGATGCCACCGTCATAGATGAATACCTAGGAAGCA
ACTCGGACGCACAAGCCAAATGCCAGGCGTTCCAGGAATTCATGGGTGACGTATTCATCAATGTTCCACCGTCA
GTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTCTATGAGTTCAGCATCGACCCAGTCTTTTG
CGAAGATCAAACCTGCCTGGGTGAAGGCTGATCGGGCCGAGGGTGCTTTTGTGTTCCGGAGGTCCCTTCCTCA
TGGACGAGAGCTCCCGCCTGGCCTTTCCAGAGGCCACAGAGGAGGAGAAGCAGCTAAGCCTCACCATGATGGCCC
AGTGGACCCACTTTGCCCGGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTTGGCCCCAATTCAACCAGGCGG
AACAAATATCTGGAGATCAACCCAGTGCCACGGGCCGGACAGAAGTTCAGGGAGGCCTGGATGCAGTCTGGTCA
AGACGCTCCCCAGCAAGATACAACAGTGGCACCAGAGAAGCAGAAGAACAGGAAGGCCAGGAGGACCTCTGAGGCC
AGGCCTGAACCTTCTTGGCTGGGGCAAACCACTCTTCAAGTGGTGGCAGAGTCCCAGCACGGCAGCCCGCCTCTC
CCCCCTGAGACTTTAATCTCCACAGCCCTTAAAGTGTGCGCCGCTCTGTGACTGGAGTTATGCTCTTTTGAA
ATGTCAACAAGCCGCTCCACCTCTGGGGCATTGTACAAGTTCTTCCCTCTCCCTGAAGTGCCTTTCCTGCTTT
CTTCGTGGTAGGTTCTAGCACATTCTCTAGCTTCTTGGAGGACTCACTCCCCAGGAAGCCTTCCCTGCCTTCTC
TGGGCTGTGCGGCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTCTGTGTCTGTCT
CCCCCTCAGAGGAGCTCTCTCAAAATGGGGATTAGCCTAACCCTACTCTGTACCCACACACAGGATCGGGTGGGA
CCTGGAGCTAGGGGGTGTGTTGCTGAGTGAAGTGAAGTGAACACAGAATATGGGAATGGCAGCTGCTGAACCTGAAC
CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCCACCACATTGTCCACCTGGCCAGAAGGGTGCATGCC
AATGGCAGAGACCTGGGATGGGAGAAGTCTGGGGCGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCCCTGAC
TAAGGCCTCAGACTAGGGCGGGAGGGGTCTCCTCCTCTCTGCTGCCAGTCTTGGCCCTGCACAAGACAACAGA
ATCCATCAGGGCCATGAGTGTACCCAGACCTGACCTCACCATTCCAGCCCCCTGACCTCAGGACGCTGGATG
CCAGCTCCCAGCCCCAGTGCCGGGTCTCCCTCCCTTCTGGCTTGGGGAGACCAGTTTCTGGGGAGCTTCCAAG
AGCACCCACCAAGACACAGCAGGACAGGCCAGGGGAGGGCATCTGGACCAGGGCATCCGTGGGGCTATTGTACA
GAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGGTGAAAAGCACAAGAGGTTTTTCAGATGGAAGTGAGAG
GTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGCTTGTCTCTCCCTGCCGCTCTGCTGGGCTCCCACTTTGGCA
GCACTTGAGGAGCCCTTCAACCCGCCGCTGCACTGTAGGAGCCCTTTCTGGGCTGGCCAAGGCCGGAGCCAGCT
CCCTCAGCTTGCAGGGGAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGCAGGGCCAG
AGTGAGTTCCGGGTGGGCGTGGGCTCGGCGGGGCCCCACTCAGAGCAGCTGGCCGGCCCCAGGCAGTGAGGGCCT
TAGCACCTGGGCCAGCAGCTGCTGTGCTCGATTCTCGCTGGGCCTTAGCTGCCTCCCCGCGGGGACGGCTCGG
GACCTGCAGCCCTCCATGCCTGACCTCCCCCCCCACCCCGTGGGCTCCTGTGCGGGCCGAGCCTCCCCAAGGAG
CGCCGCCCCCTGCTCCACAGCGGCCAGTCCCATCGACCACCCAAGGGCTGAGGAGTGCGGGTGACAGCGCGGGA
CTGGCAGGCAGCTCCACCTGCTGCCCCAGTGTGGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGG
GGACTTGAGAAACCTTTATGTCTAGCTAAGGGATTGTAAATACCCGATGGGCACTCTGTATCTAGCTCAAGGTT
TGTAACACACCAATCAGCACCTGTGTCTAGCTCAGTGTGTTGTGAATGCACCAATCCACACTGTGTATCTGGCT
ACTCTGGTGGGACTTGGAGAACCTTTGTGTCCACACTGTATCTAGCTAATCTAGTGGGATGTGGAGAACCT
TTGTGTCTAGCTAGGATCGTAAACGCACCAATCAGCACCTGTCAAACAGACCACTTGACTCTGTGTAAGT
GGACCAATCAGCAGGATGTGGGTGGGGCGAGACAAGAGAATAAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCC
CCCTCGGGTCCCTCCACGCGCTGGAAGCTTTGTTCTTTCGCTCTTTGCAATAAATCTTGCTACTGCCAAAA

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FIGURE 542

MERAVRVESGVLVGVVCLLLACPATATGPEVAQPEVDTTLGRVRGRQVGVKGTDRLVNVFLGI
PFAQPPPLGPDRFSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDCLV
LNVYSPA EVPAGSGRPVMVWVHGGALITGAATSYDGSALAA YGDVVVVTVQYRLGVLGFFSTG
DEHAPGNQGF LDVVAALRWVQENIAPFGGDLNCVTVFGGSAGGSIISGLVLS PVAAGLFHRAI
TQSGVITTPGII DSHPWPLAQK IANTLACSSSSPAEMVQCLQQKEGEELVLSKKLKNTIYPLT
VDGTVFPKSPKELLKEKPFH SVPF LMGVNNHEFSWLI PRGWGLLDTMEQMSREDMLAISTPVL
TSLDVPP EMMPTVIDEYLG SNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGSPVFFYEF
QHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTMMAQWTHFA
RTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLP SKIQQWHQKQKNRKA
QEDL

Important features:**Signal peptide:**

amino acids 1-27

Transmembrane domain:

amino acids 226-245

N-glycosylation site.

amino acids 105-109

N-myristoylation sites.

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,
461-467

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23

Carboxylesterases type-B serine active site.

amino acids 216-232

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FIGURE 543

TGTCGCCTGGCCCTCGCCATGCAGACCCCGCGAGCGTCCCCTCCCCGCCCCGGCCCTCCTGCTTCTGCTGCTGCTA
CTGGGGGGCGCCACGGCCTCTTCTGAGGAGCCGCCGCGCTTAGCGTGGCCCCCAGGGACTACCTGAACCAC
TATCCCGTGTGTTTGTGGGCAGCGGGCCCGACGCCTGACCCCGCAGAAAGGTGCTGACGACCTCAACATCCAGCGA
GTCTTGGGGTCAACAGGACGCTGTTTATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCAGC
TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAAACGTGTGTGCGATGAAG
GGCAAACAGGAGGGCGAGTGTGAAACTTCGTAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC
GGTATGGCCCGCTGCCCCGTACGACCCCAAGCAGCCCAATGTTGCCCTCTTCTCTGACGGGATGCTCTTCACAGCT
ACTGTTACCGACTTCCTAGCCATTGATGCTGTCTATCTACCGCAGCCTCGGGGACAGGCCACCCTGCGCACCCGTG
AAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTTC
TTCCGGGAGATTGCGATGGAGTTTAACTACCTGGAGAAGGTGGTGGTGTCCGCGTGGCCCCGAGTGTGAAGAAC
GACGTGGGAGGCTCCCCCGCGTGTGGAGAAGCAGTGGACGTCCTTCCTGAAGGCGCGGCTCAACTGCTCTGTA
CCCGGAGACTCCCATTCTACTTCAACGTGCTGCAGGCTGTACGGGGCGTGGTACGCTCGGGGGCGGGCCCGTG
GTCCTGGCCGTTTTTTTCCACGCCAGCAACAGCATCCCTGGCTCGGCTGTCTGCGCCTTTGACCTGACACAGGTG
GCAGCTGTGTTTGAAGGCCGCTTCCGAGAGCAGAAGTCCCCGAGTCCATCTGGACGCCGGTGCCGGAGGATCAG
GTGCCTCGACCCCGGGCCCGGTGCTGCGCAGCCCCCGGGATGCAGTACAATGCCTCCAGCGCCTTGCCGGATGAC
ATCCTCAACTTTGTCAAGACCCACCCTCTGATGGACGAGGCGGTGCCCTCGCTGGGCCATGCGCCCTGGATCCTG
CGGACCCTGATGAGGCACACAGCTGACTCGAGTGGCTGTGGACGTGGGAGCCGGCCCCCTGGGGCAACCAGACCGTT
GTCTTCTTGGGTTCTGAGGCGGGGACGGTCCCTCAAGTTCCTCGTCCGGCCCAATGCCAGCACCTCAGGGACGTCT
GGGCTCAGTGTCTTCTGGAGGAGTTTGAGACCTACCGGCCGGACAGGTGTGGACGGCCCGGGCGGTGGCGAGACA
GGGCAGCGGCTGCTGAGCTTGGAGCTGGACGCAGCTTCGGGGGGCCTGCTGGCTGCCTTCCCCGCTGCGTGGT
CGAGTGCCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTCAGGACCCCTACTGC
GGGTGGGGCCCCGACGGCTCCTGCATCTTCTCAGCCCGGGCACCAGAGCCGCTTTGAGCAGGACGTGTCCGGG
GCCAGCACCTCAGGCTTAGGGGACTGCACAGGACTCCTGCGGGCCAGCCTCTCCGAGGACCGCGCGGGGCTGGTG
TCGGTGAACCTGCTGGTAACGTGCTCGGTGGCGGCCTTCGTGGTGGGAGCCGTGGTGTCCGGCTTCAGCGTGGG
TGGTTCGTGGGCCTCCGTGAGCGCGGGAGCTGGCCCGGCCGCAAGGACAAGGAGGCCATCCTGGCGCACGGGGCG
GGCGAGGCGGTGCTGAGCGTCAGCCGCTGGGCGAGCGCAGGGCGCAGGGTCCCGGGGGCGGGGGCGGAGGCGGT
GGCGGTGGCGCGGGGTTCCCCCGAGGGCCCTGCTGGCGCCCTGATGCACAACGGCTGGGCCAAGGCCACGCTG
CTGCAGGGCGGGCCCCACGACCTGGACTCGGGGTGCTGCCACGCCCCGAGCAGACGCCGCTGCCGCGAAGCGC
CTGCCCCACTCCGCACCCGCACCCCCACGCCCTGGGCCCCCGCGCCTGGGACCACGGCCACCCCCCTGCTCCCGGCC
TCCGCTTATCTCCCTCCTGCTGCTGGCGCCCGCCGGGCCCGGAGCAGCCCCCGCGCCTGGGGAGCCGACC
CCCGACGGCCGCTCTATGCTGCCCGGCCCGCGCCTCCACAGGCGACTTCCCGCTACCCCCCACGCCAGC
CCGACCGCCGCGGGTGGTGTCCGCGCCACGGGCCCTTGACCCAGCCTCAGCCGCCGATGGCCTCCCGCGG
CCCTGGAGCCCGCCCCGACGGGCAGCCTGAGGAGGCCACTGGGCCCCACGCCCTCCGGCCGCCACCCTGCGC
CGCACCCACAGTTTAAACAGCGCGGAGGCCCGGCCCTGGGGACCGCCACCGCGCTGCCACGCCCGGCCGGGACA
GACTTGGCCACCTCCTCCCCATATGGGGGGGGGACAGGACTGCGCCCCCGTGCCCTAGGCCGGGGGCCCCCG
ATGCCCTTGGCAGTGCCAGCCACGGGAACCAGGAGCAGAGACGGTGCCAGAACGCCGGGGCCGGGGCAACTCCG
AGTGGGTGCTCAAGTCCCCCGCGACCCACCCGCGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACAAACAG
CTCGCCCTCCCCCTACCCGGGGCCGACAGGACGCTGAGACGGTTTGGGGGTGGGTGGGCGGGAGGACTTTGCTATG
GATTTGAGGTTGACCTTATGCGCGTAGGTTTTTGGTTTTTTTTTGCAGTTTTGGTTTTCTTTTGGGTTTTCTAACC
AATTGCACAACCTCCGTTCTCGGGGTGGCGGCAGGCAGGGGAGGCTTGGACCCGGTGGGGAATGGGGGGCCACAG
CTGCAGACCTAAGCCCTCCCCACCCCTGGAAGGTCCCTCCCCAACCCAGGCCCTGGCGTGTGTGGGTGTGCG
TGCGTGTGCGTGCCGTGTTCTGTGTGAAGGGGCGGGGAGGTGGGCGTGTGTGTGCGTGCCAGCGAAGGCTGCTG
TGGGCGTGTGTGTCAAGTGGGCCACGCGTGCAGGGTGTGTGTCCACGAGCGACGATCGTGGTGGCCGACGCGCC
TGGGCGTGTGTGTGAGCCGACGCTGGGGCTTCCAGAAGGCCCGGGGTCTCCGAGGTGCCGGTTAGGAGTTTGAAC
CCCCCCCCCTCTGCAGAGGGAAGCGGGGACAATGCCGGGGTTTTCAGGCAGGAGACACGAGGAGGGCCTGCCCGGA
AGTCACATCGGCAGCAGCTGTCTAAAGGGCTTGGGGGCTGGGGGGCGGCGAAGGTGGGTGGGGCCCCCTCTGTAA
ATACGGCCCCAGGGTGGTGAGAGAGTCCCATGCCACCCGTCCTTGTGACCTCCCCCTATGACCTCCAGCTGA
CCATGCATGCCAGTGCTGGTGGTCTGCTGCTCTTGGAGTTTGCTCCCCAGCCCCCTCCCCATCAAT
AAAACCTCTGTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 544

MQTPRASPPRPALLLLLLLLGGAGHLFPPEPPPLSVAPRDYLNHYPVFVGSGPGRLTPAEGAD
 DLNIQRVLRVNRTLFIGDRDNLRYVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEGEC
 RNFVKVLLLRDESTLFVCGSNAFNPVCANYSIDTLQPVGDNISGMARCPYDPKHANVALFSDG
 MLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGSHVYFFFREIAMEF
 NYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGD SHFYFNVLQAVTGVVSLG
 GRPVVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESIWTPVPEDQVPRPRPGCC
 AAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLG HAPWILRTLMRHQLTRVAVDVGAGPWGN
 QTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYRPDRCGRPGGGETGQRLLSLELD
 AASGGLLAAPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDGSCIFLSPGTRAAFEQDV
 SGASTSGLGDCGTGLLRASLSEDRAGLVSVNLLVTSSVAAFVVGAVVSGFSVGVFWGLRERREL
 ARRKDKEAILAHGAGEAVLSVSR LGERRAQGGGRRGGGGGGGAGVPPEALLAPLMQNGWAKAT
 LLQGGPHDLD SGLLPTPEQTPLPQKRLPTPHPHPHALGPRAWDHGHPLLPASASSSLLLLAPA
 RAPEQPPAPGEPTPDGRLYAARPGRASHGDFLTPHASPDRRRRVVSAPTGPLDPASAADGLPR
 PWSPPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPGTDLAHL LPYGGADR
 TAPPVP

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 318-339, 598-617

N-glycosylation sites.

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,
462-466

Glycosaminoglycan attachment sites.

amino acids 51-55, 573-577

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106.

N-myristoylation sites.

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,
668-674, 669-675, 670-676, 868-874, 879-885

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FIGURE 545

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCGCCAAA
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCCTCTAGT
CTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCCACATGACA
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAG
GAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGATTGTCTTTATGCATCCCC
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTTTCTGCTATTGGATATATT
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT
ACAGTAAAAAAAACCTTGTAATCTAGAAGAGTGGCTAGGGGGGTATTTCATTTGTAT
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC
TACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 546

MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNGATT CATNSHSDSEL RPE
IFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAFYLLWTPSTGLKTLNLGSCVIATNLQE
IRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHY
TLRKISSLAN SFLT IKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQA AVVKALGELDI
LLQWMEETE

Important features:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

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FIGURE 547

AGCAACTCAAGTTCATCATTGTCCTGAGAGAGAGGAGCAGCGCGGTTCTCGGCCGGGACAGCA
GAACGCCAGGGGACCCTCACCTGGGCGCGCCGGGGCACGGGCTTTGATTGTCCTGGGGTTCGCG
GAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTGCGA
TCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTCATTT
ATCGGTGGATCATTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATTGCTTC
TTTCTGGCGACAGTTCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCGGAGAAG
AGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCCTTCCCGCCCGCTATTTCTATATT
CAGGCAGTGGATACATCAGGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCTTCCAGGTG
AAAGTCTCAGCACCAGAGGAGCAATTCACTAGAGTTGGAGTCCAGGTTTTAGACCGAAAAGAT
GGTCTTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAAATCTGAAGGTGGAAATTAAA
TTCCAAGGGCAACATGTGGCCAAATCCCATATATTTTAAAAGGGCCGGTTTACCATGAGAAC
TGTGACTGTCCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGCCCTGAAACCATT
GCTCAGATTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAAGATTGCAGTAGAA
ATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAAAGGATAACAAGGT
TATATCAAGACTCATGGTGAACATGTAGGTTTTAGAAATTTTCATGGATGCCATACTACTTTCT
TTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTTGGGAGACTGGCCTTTG
GAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCCTGGTGTGGCTCCACAGATTCC
AAGGATATCGTGATGCCTACGTACGATTTGACTGATTCTGTTCTGGAAACCATGGGCCGGGTA
AGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCCCTCCCTGGGAAAGCAAAAATTCCTACT
GCCGTCTGGAGAGGGCGAGACAGCCGCAAAGAGAGACTCGAGCTGGTTAAACTCAGTAGAAAA
CACCCAGAACTCATAGACGCTGCTTTCACCAACTTTTTCTTCTTTAAACACGATGAAAACCTG
TATGGTCCCATTGTGAAACATATTTCAATTTTTTGATTTCTTCAAGCATAAGTATCAAATAAAT
ATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGCTAGTTGGTGACAGTGTGTGCTG
AAGCAGGATTCCATCTACTATGAACATTTTTACAATGAGCTGCAGCCCTGGAAACACTACATT
CCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAAACTTAAATGGGCGAAAGATCACGATGAA
GAGGCCAAAAAGATAGCAAAAGCAGGACAAGAATTTGCAAGAAATAATCTCATGGGCGATGAC
ATATTCTGTTATTATTTCAAACCTTTCCAGGAATATGCCAATTTACAAGTGAGTGAGCCCCAA
ATCCGAGAGGGCATGAAAAGGGTAGAACCACAGACTGAGGACGACCTCTTCCCTTGTAATTGC
CATAGGAAAAAGACCAAGATGAACTCTGATATGCAAAATAACTTCTATTAGAATAATGGTGC
TCTGAAGACTCTTCTTAACTAAAAAGAAGAATTTTTTTAAGTATTAATTCCATGGACAATATA
AAATCTGTGTGATTGTTTGCAGTATGAAGACACATTTCTACTTATGCAGTATTCTCATGACTG
TACTTTAAAGTACATTTTTTAGAATTTTATAATAAAACCACCTTTATTTTAAAGGAAAAAAA

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FIGURE 548

MFGTLLLYCFFLATVPALAETGGERQLSPEKSEIWGPGLKADVVLPAFYFYIQAVDTSGNKFT
SSPGEKVFQVKVSAPEEQFTRVGQVLDKDGSEFIVRYRMYASYKNLKVEIKFQGQHVAKSPY
ILKGPVYHENCDCPLQDSAALWREMNCPETIAQIQDLAHFPAVDPEKIAVEIPKRFGQRQSL
CHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRKVKMPDVELFVNLDGWPLEKKKSNSNIHP
IFSWCGSTDSDKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGRDSRKE
RLELVKLSRKHPOLIDAAFTNFFFFKH DENLYGPIVKHISFFDFFKH KYQINIDGTVAAYRLP
YLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKSNSLDLLEKLKWAKDHDEEAKKIAKAGQE
FARNNLMGDDIFCYF KLFQ EYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRKKTKDEL

Important features:**Signal peptide:**

amino acids 1-17

N-glycosylation sites.

amino acids 302-306, 414-418

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 243-247, 495-499

Tyrosine kinase phosphorylation site.

amino acids 341-348

N-myristoylation sites.

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

Endoplasmic reticulum targeting sequence.

amino acids 499-504

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FIGURE 549

GGGTGATTGAACTAAACCTTCGCCGCACCGAGTTTGCAGTACGGCCGTCACCCGCACCGCTGC
CTGCTTGCGGTTGGAGAAATCAAGGCCCTACCGGGCCTCCGTAGTCACCTCTCTATAGTGGGC
GTGGCCGAGGCCGGGGTGACCCTGCCGGAGCCTCCGCTGCCAGCGACATGTTCAAGGTAATTC
AGAGGTCCGTGGGGCCAGCCAGCCTGAGCTTGCTCACCTTCAAAGTCTATGCAGCACCAAAAA
AGGACTCACCTCCCAAAAATTCGCTGAAGGTTGATGAGCTTTCCTCTACTCAGTTCCTGAGG
GTCAATCGAAGTATGTGGAGGAGGCAAGGAGCCAGCTTGAAGAAAGCATCTCACAGCTCCGAC
ACTATTGCGAGCCATACACAACCTGGTGTGTCAGGAAACGTA CTCCCAAATAAGCCCAAGATGC
AAAGTTTGGTTCAATGGGGGTTAGACAGCTATGACTATCTCCAAAATGCACCTCCTGGATTTT
TTCCGAGACTTGGTGTTATTGGTTTTGCTGGCCTTATTGGACTCCTTTTGGCTAGAGGTTCAA
AAATAAAGAAGCTAGTGTATCCGCCTGGTTTCATGGGATTAGCTGCCTCCCTCTATTATCCAC
AACAAGCCATCGTGTTTGCCAGGTCAGTGGGGAGAGATTATGACTGGGGTTTACGAGGAT
ATATAGTCATAGAAGATTTGTGGAAGGAGAACTTTCAAAGCCAGGAAATGTGAAGAATTCAC
CTGGAATAAGTAGAAAACTCCATGCTCTGCCATCTTAATCAGTTATAGGTAAACATTGGAAA
CTCCATAGAATAAATCAGTATTTCTACAGAAAAATGGCATAGAAGTCAGTATTGAATGTATTA
AATTGGCTTTCTTCTTCAGGAAAACTAGACCAGACCTCTGTTATCTTCTGTGAAATCATCCT
ACAAGCAAATAACCTGGAATCCCTTCACCTAGAGATAATGTACAAGCCTTAGAACTCCTCAT
TCTCATGTTGCTATTTATGTACCTAATTAAACCCAAGTTTAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 550

MFKVIQRSVGPASLSLLTFKVYAAPKKDSPPKNSVKVDELSLYSVPEGQSKYVEEARSQLEES
ISQLRHYCEPYTTWCQETYSQTKPKMQSLVQWGLDSYDYLQNAPPGFFPRLGVIGFAGLIGLL
LARGSKIKKLVYPPGFMGLAASLYYPQQAIVFAQVSGERLYDWGLRGYIVIEDLWKENFQKPG
NVKNSPGTK

Important features:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 111-130

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 36-44

N-myristoylation sites:

Amino acids 124-130;144-150;189-195

